

US007759461B2

(12) **United States Patent**
Chen et al.

(10) **Patent No.:** **US 7,759,461 B2**
(45) **Date of Patent:** **Jul. 20, 2010**

(54) **EXPRESSION SYSTEM FOR ENHANCING SOLUBILITY AND IMMUNOGENEICITY OF RECOMBINANT PROTEINS**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 97 days.

(21) Appl. No.: **12/406,789**

(22) Filed: **Mar. 18, 2009**

(65) **Prior Publication Data**
US 2009/0187004 A1 Jul. 23, 2009

Related U.S. Application Data
(62) Division of application No. 12/149,606, filed on May 5, 2008, now Pat. No. 7,524,648.

(30) **Foreign Application Priority Data**
May 4, 2007 (TW) 96115989 A

(51) **Int. Cl.**
C07K 1/00 (2006.01)

(52) **U.S. Cl.** **530/350**

(58) **Field of Classification Search** **530/350**
See application file for complete search history.

(56) **References Cited**

OTHER PUBLICATIONS

No references cited.*

* cited by examiner

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(57) **ABSTRACT**

Expression system for enhancing solubility and immunogenicity of recombinant proteins. The expression system includes a protein expression vector that contains a chimeric gene encoding a chimeric protein comprising: (a) a first polypeptidyl fragment at the N-terminal end of the chimeric protein, containing a protein transduction domain (PTD), or a fragment thereof, having HIV Tat PTD activity; (b) a second polypeptidyl fragment at the C-terminal end of the first polypeptidyl fragment, containing a J-domain, or a fragment thereof, having heat shock protein 70 (Hsp70)-interacting activity; and (c) a third polypeptidyl fragment at the C-terminal end of the second polypeptidyl fragment, containing a target protein or polypeptide.

4 Claims, 15 Drawing Sheets

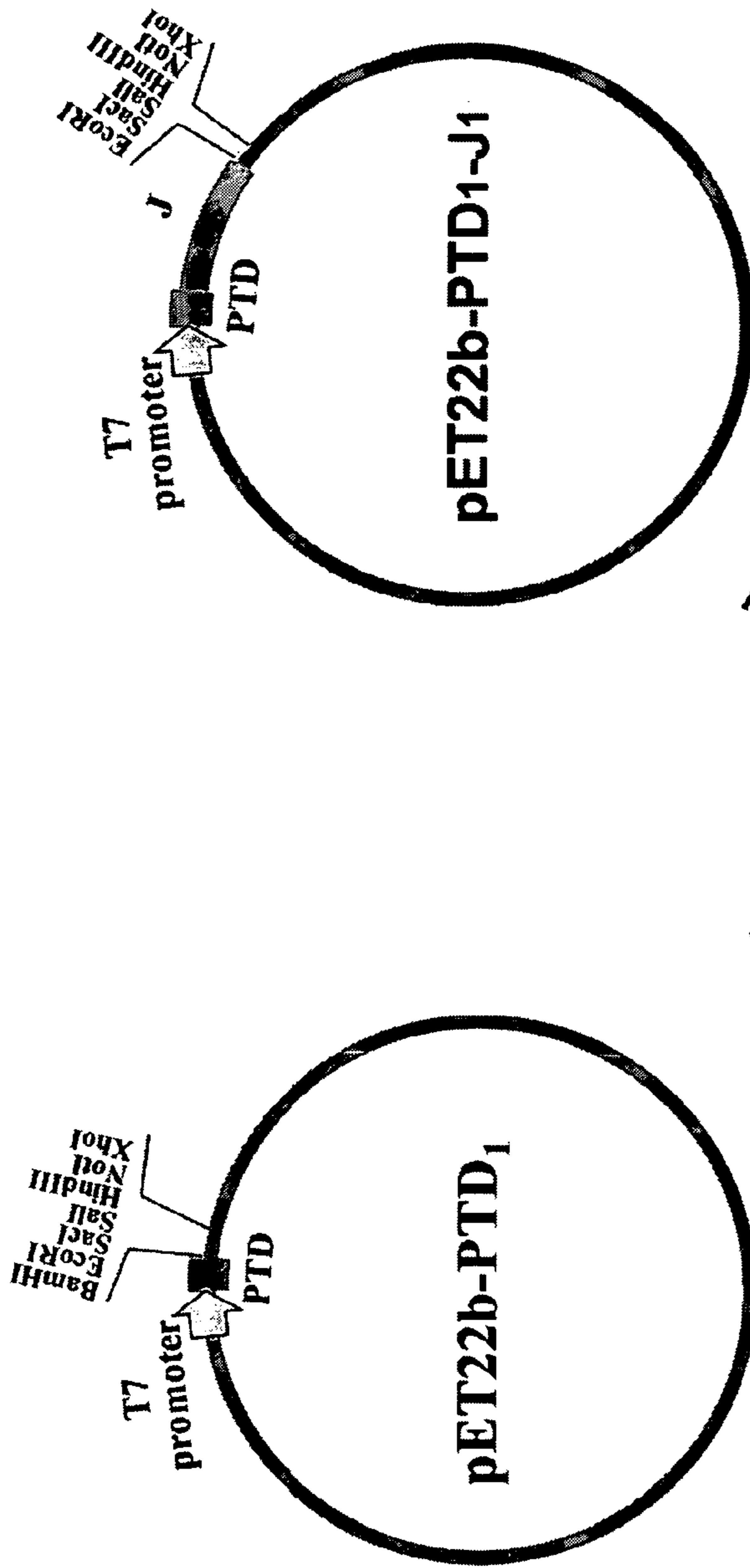


FIG. 1A

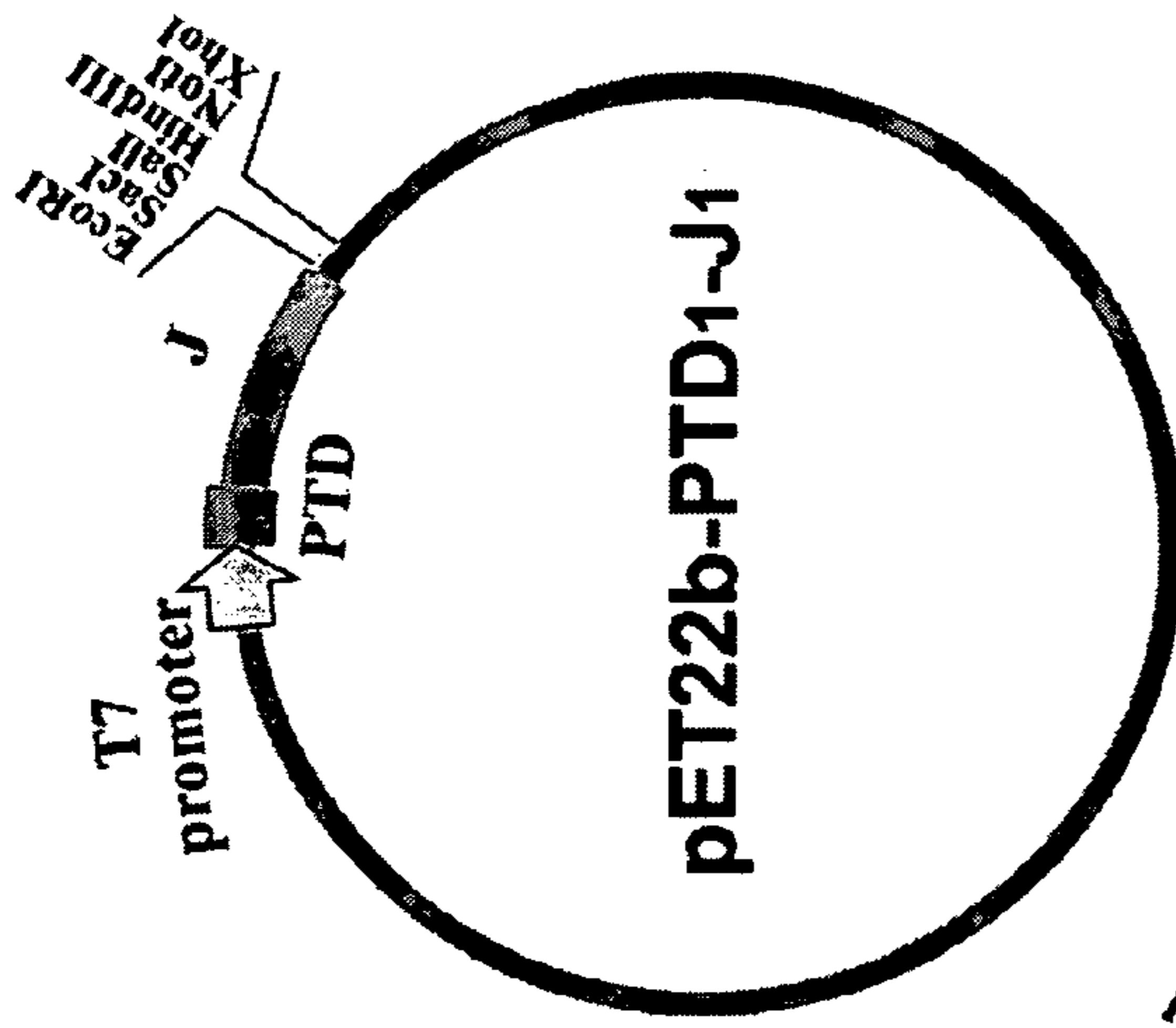


FIG. 1B

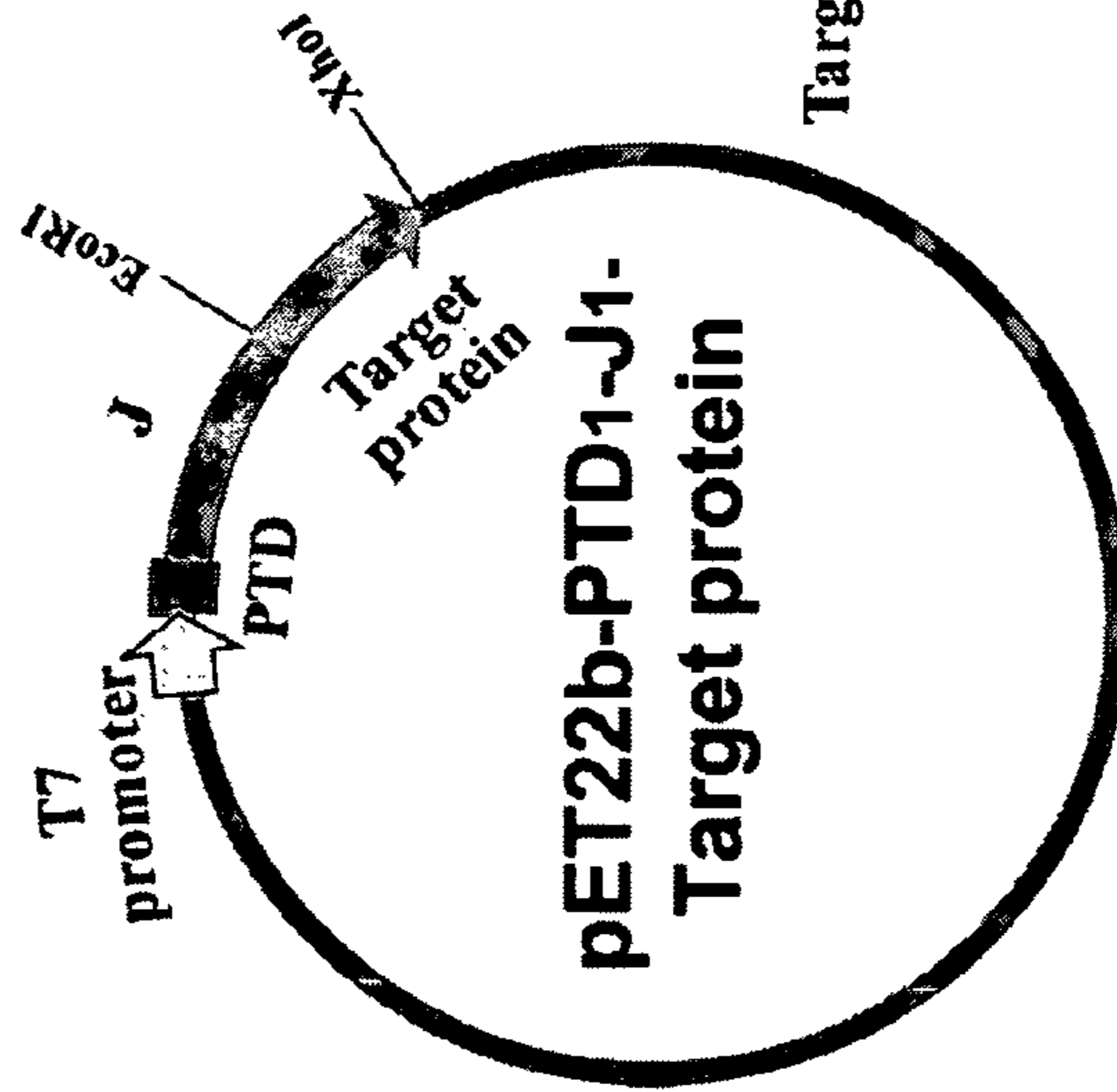


FIG. 1C

Target protein = HSPA1A peptide I
Hp-NC
cIGF-I
...etc.

pET-22b-PTD₁

AGATCT CGATCCCGCGGAAAT TAAATACGACTCACTAT AGG GGAATTGTGAGCCGGATAACAATTC C C TCTAGA AATAATTTTGTTTAACTTTTAA
 17 primer
 17 primer
 lac operator
 XbaI

NdeI
 CTTTAGAAGGAG ATATA CAT ATG TAT GGT CGT AAG AAA CGT CGT CAG CGT CGT CGT GTG
 Met Tyr Gly Arg Lys Lys Arg Arg Arg Gln Arg Arg Arg Val
 rib

BamHI EcoRI SacI SalI HindIII NotI XhoI
 GGG ATC CG AAT TCG AGC TCC GTC GAC AAG CTT GCG GCC GCA CTC GAG
 Gly Ile Asn Ser Ser Ser Val Asp Lys Leu Ala Ala Ala Leu Glu

CAC CAC CAC CAC CAC TGA GATCCGGCTGCTAACAAAGCCGAAAGGAGCTGAGTTGGCTGCCACCCTGAGCAATAA
 His His His His His His stop
 His-tag

CTAGCATACCCCTTGGGCTCTAAACGGCTCTGAGGGGTTTTG
 17 terminator

FIG. 2A

pET-22b-PTD₁-J₁

AGATCT CGATCCCGCGAAT TATATCCACTCACTAT AGG GGAATTGTGAGCCGGATACACATTC CC TCTAGA AATAATTTTGTTAAC TTAA
T7 primer
GGG ATC CTC GGT AAA GAT TAC TAC CAG ACF CAC GGT CTC GGT GCA TCT GAT GAT GAA ATC AAA CSE GCF TAC GCF CAG GCA CTG CCF TAC
T7 promoter *lac operator* *XbaI*
CTTAAAGAGGAG ATATA CAT ATG TAT GGT CGT AAG AAA CGT CGT CAG CGT CGT CGT GTG

rib *NdeI*
Met Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Val

BamHI
GGG ATC CTC GGT AAA GAT TAC TAC CAG ACF CAC GGT CTC GGT GCA TCT GAT GAT GAA ATC AAA CSE GCF TAC GCF CAG GCA CTG CCF TAC
 Gly Ile Leu Gly Lys Asp Tyr Tyr Gln Thr His Gly Leu Ala Arg Gly Ala Ser Asp Asp Gln Ile Lys Arg Ala Tyr Arg Arg Gln Ala Leu Arg Tyr

GAT CCA GAC AAR AAC AAA GAA CCG GGT GCA GAA AAA TTC AAA GAG AAT CCA GAA TAC GAC GAT CCA CCF AAA CCF GAA ATC TTC
 His Pro Asp Lys Asn Lys Glu Pro Arg Ala Glu Glu Lys Phe Lys Glu Ile Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Arg Lys Arg Glu Ile Phe

GAC CCF TAC GGT GAA GAA GGT CTC AAA GGT GGT TCT GGT GGT GC
 Asp Arg Tyr Gly Glu Glu Gly Leu Lys Gly Ser Gly Gly Ala

EcoRI *SacI* *SalI* *HindIII* *NdeI* *XhoI*
G AAT TCG AGC TCC GTC GAC AAC CTT GCG GCC GCA CTC GAG
 Asn Ser Ser Ser Val Asp Lys Leu Ala Ala Ala Ala Leu Glu

CAC CAC CAC CAC CAC TGA GATCCGGCTGCTAACAAAGCCCGAAGGAGCTGAGTTGGCTGCCACCCGCTGAGCAATAA
His His His His His His stop
His-tag

CTAGCATACCCCTTGGGGCTCTAAAGCGGCTCTGAGGGGTTTTT
T7 terminator

FIG. 2B

Assembly PCR

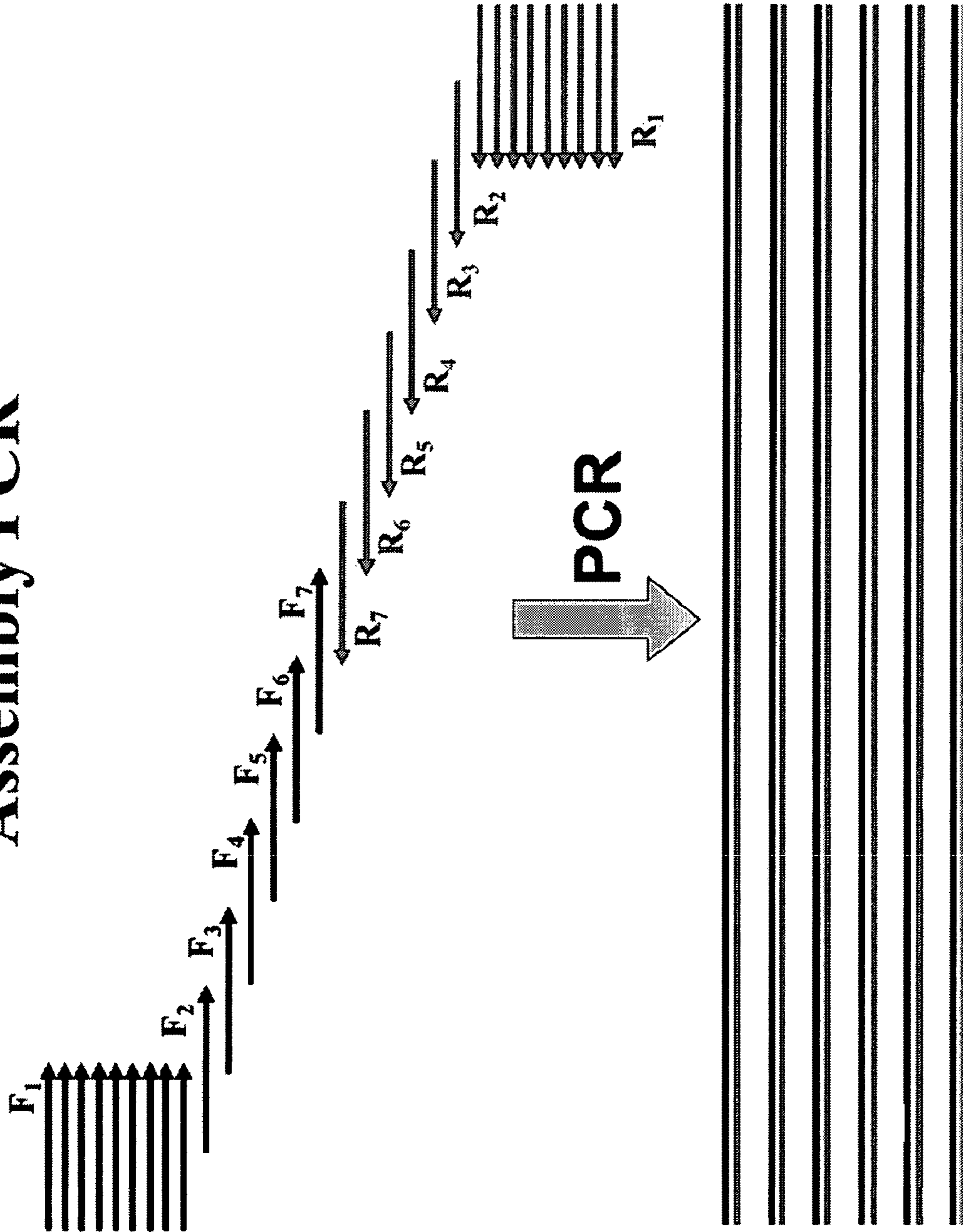


FIG. 3

PTD1-J1-HSPA1A Peptide I

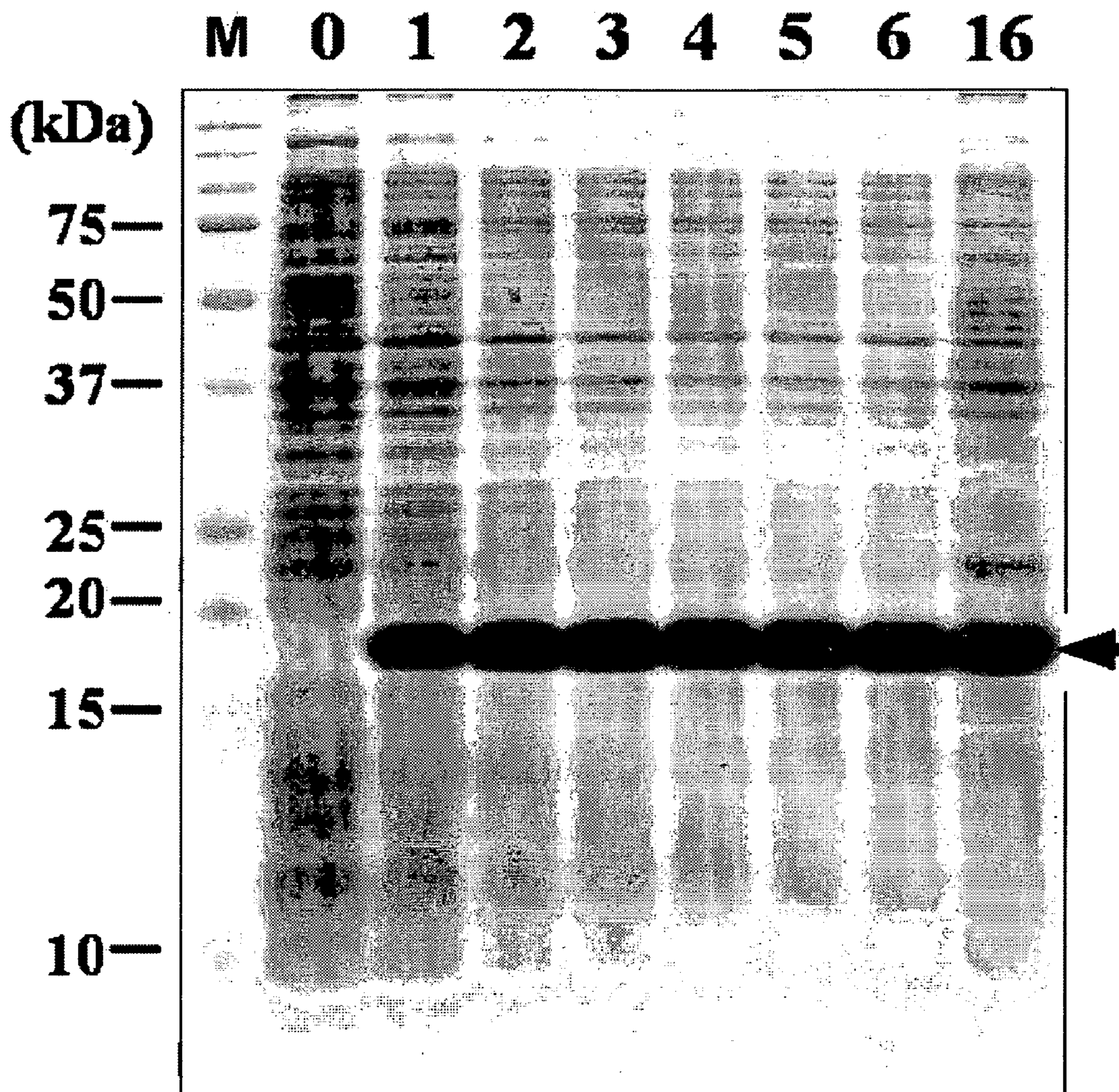


FIG. 4A

IPTG Induction Period (hr)	1	2	3	4	5	6	16
Recombinant Protein / Total Proteins (% w/w)	65	85	89	91	92	92	77

FIG. 4B

PTD1-J1-HSPA1A Peptide II

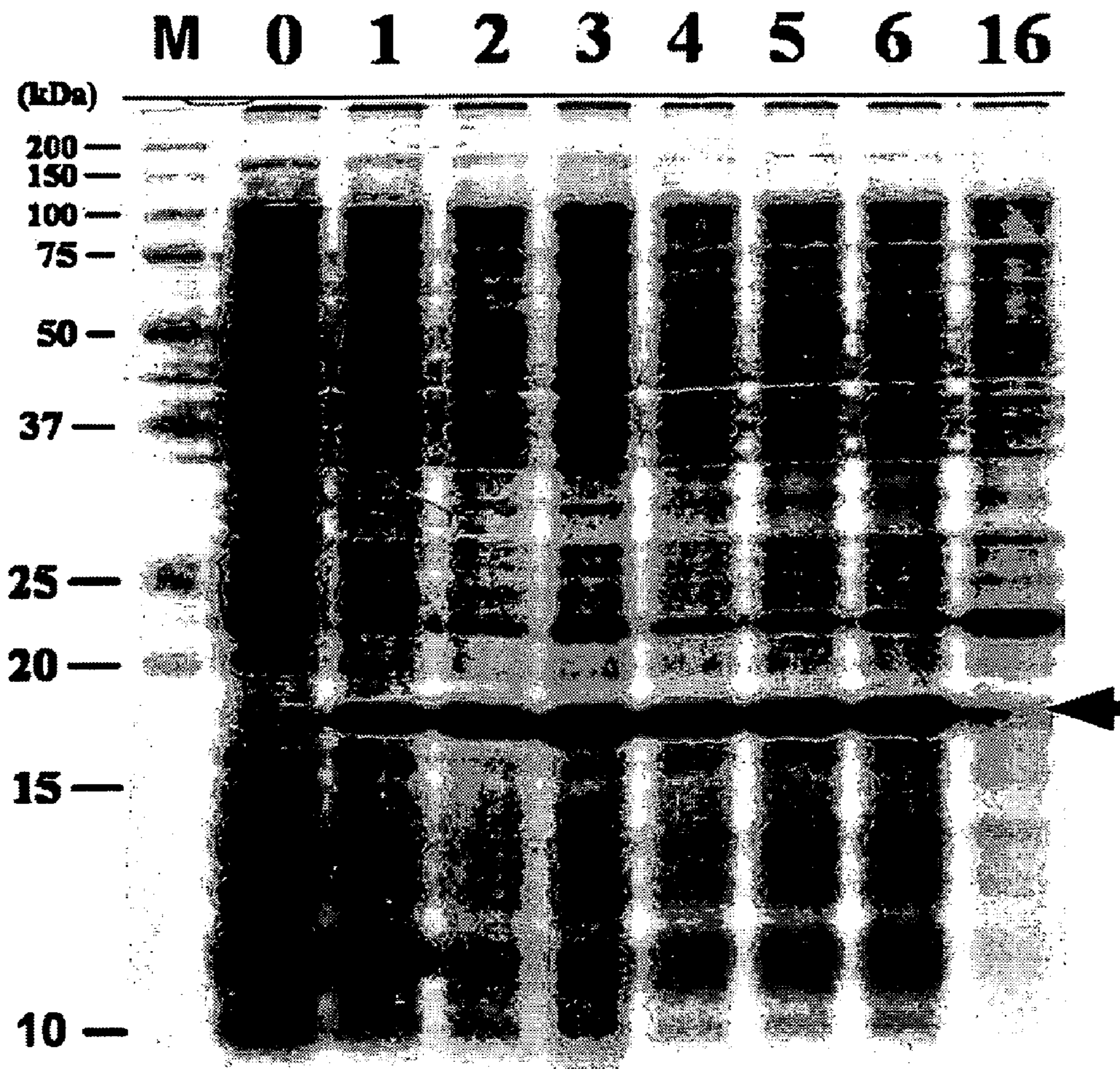


FIG. 5A

IPTG Induction Period (hr)	1	2	3	4	5	6	16
Recombinant Protein / Total Proteins (% w/w)	27	45	37	54	51	46	10

FIG. 5B

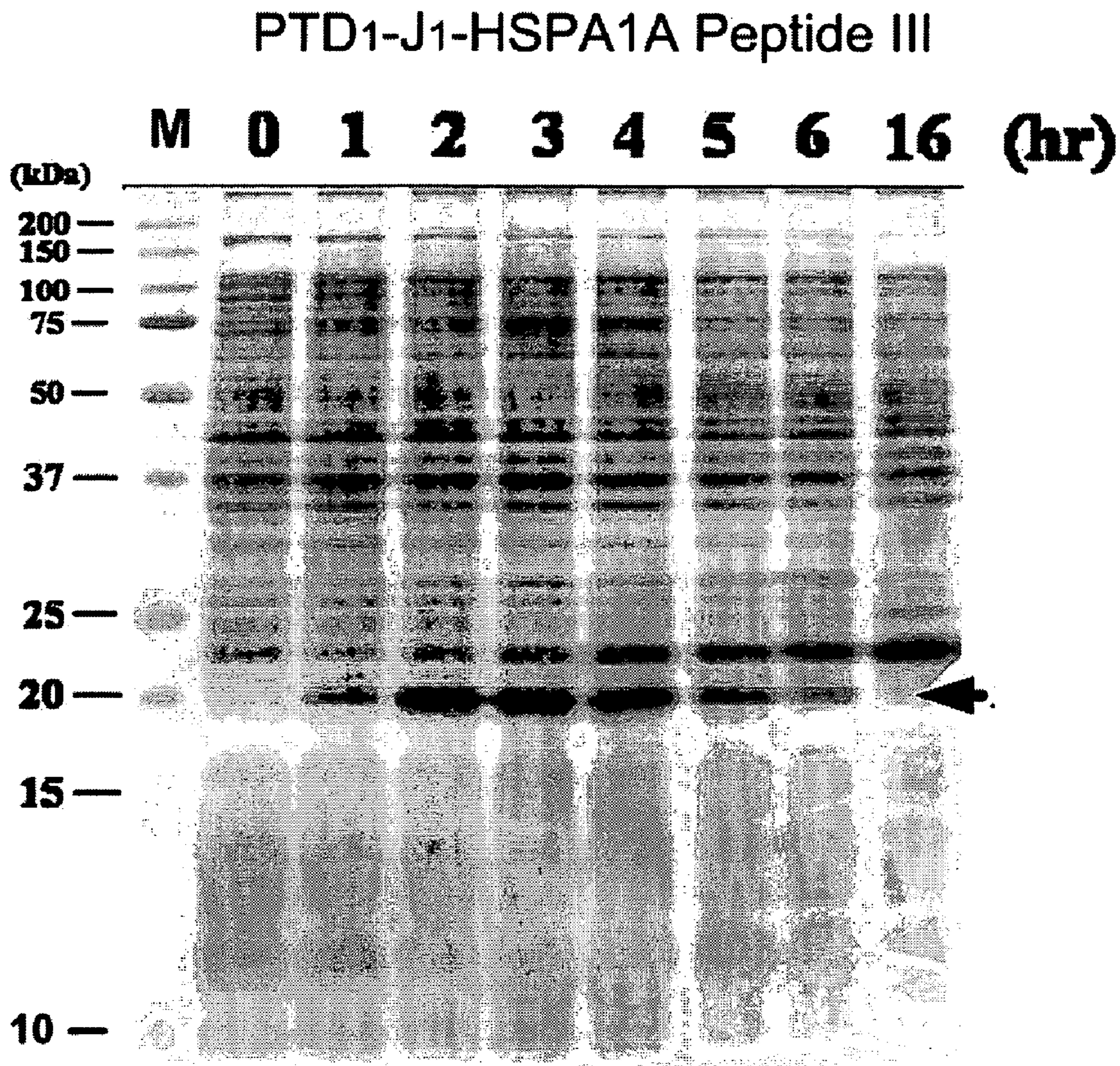


FIG. 6A

IPTG Induction Period (hr)	1	2	3	4	5	6	16
Recombinant Protein / Total Proteins (% w/w)	16	33	30	27	10	-	-

FIG. 6B

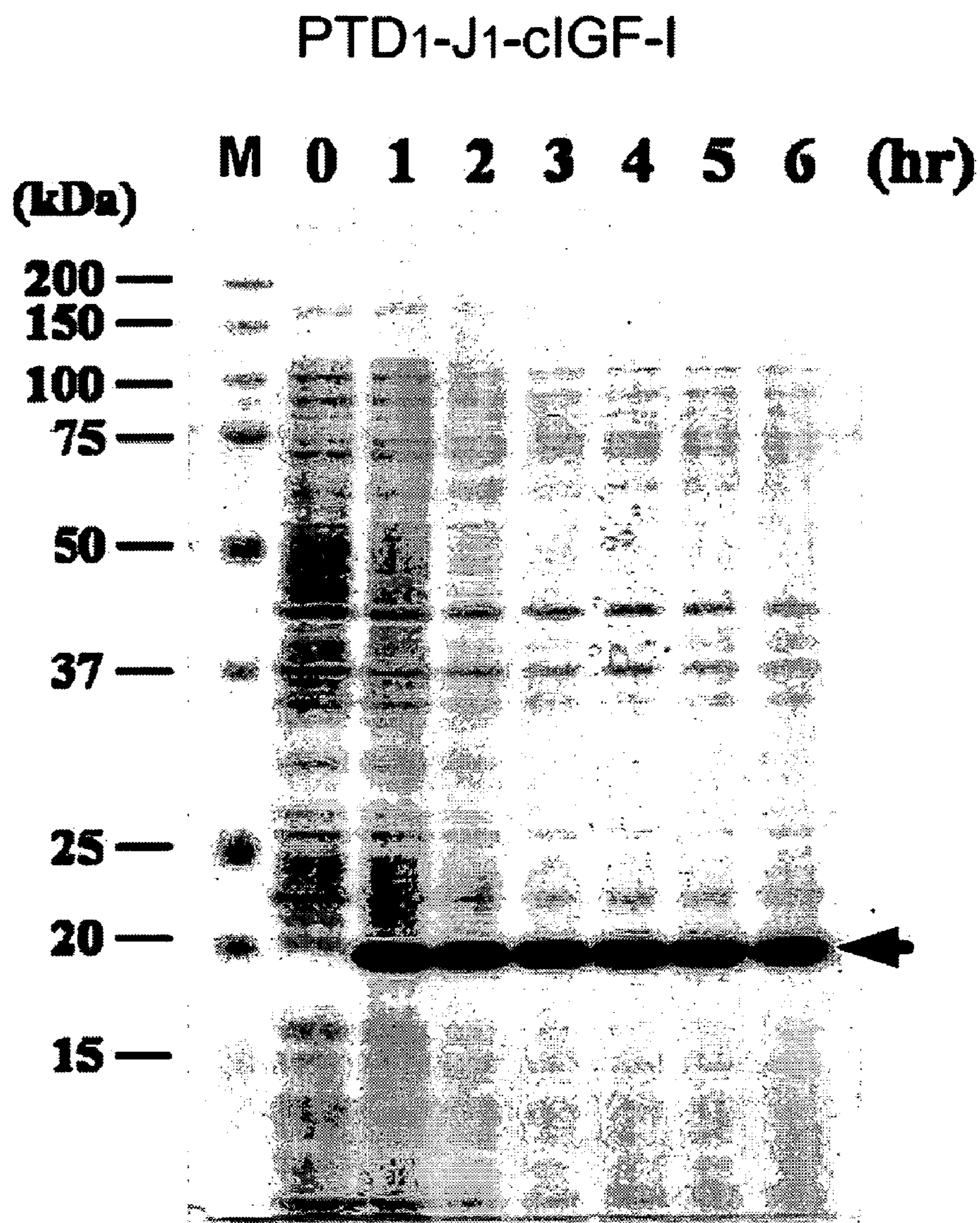


FIG. 7A

IPTG Induction Period (hr)	1	2	3	4	5	6
Recombinant Protein / Total Proteins (% w/w)	74	87	89	90	90	90

FIG. 7B

PTD1-J1-HA_RBD

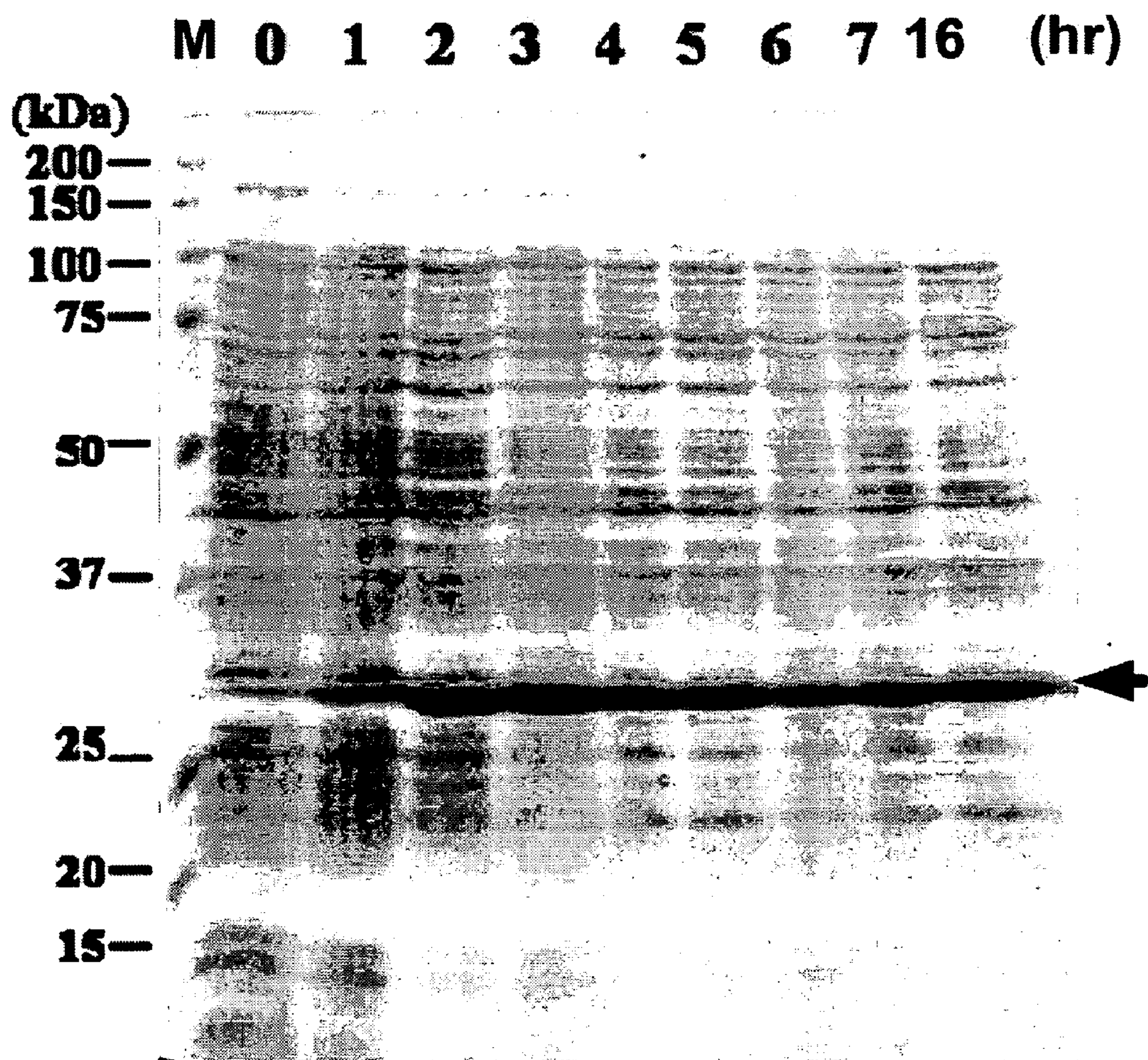


FIG. 8A

IPTG Induction Period (hr)	1	2	3	4	5	6	7	16
Recombinant Protein / Total Proteins (% w/w)	12	31	38	28	32	27	34	32

FIG. 8B

PTD1-J1-HCV-core protein (1 to 171)

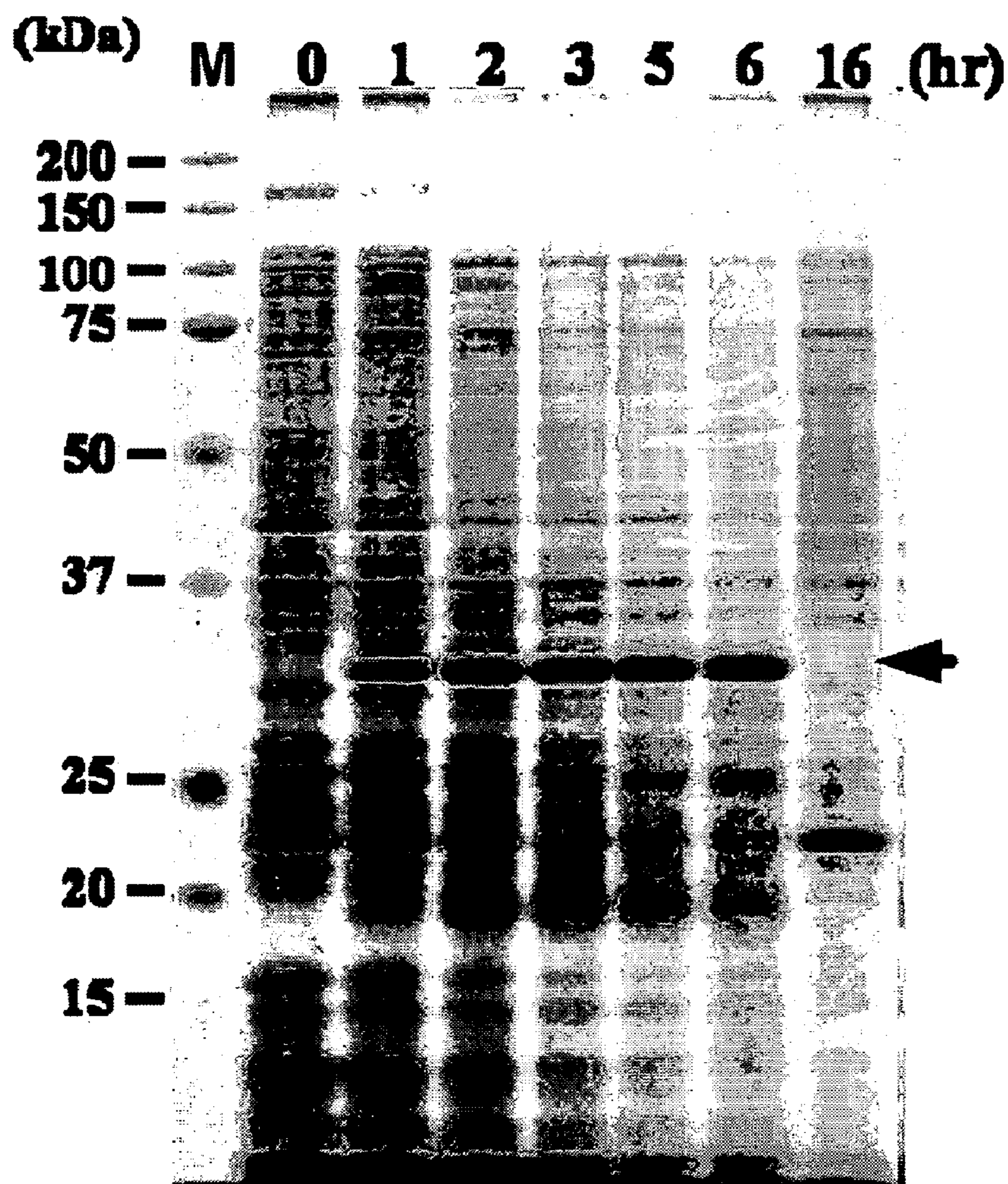


FIG. 9A

IPTG Induction Period (hr)	1	2	3	5	6	16
Recombinant Protein / Total Proteins (% w/w)	11	25	31	36	39	-

FIG. 9B

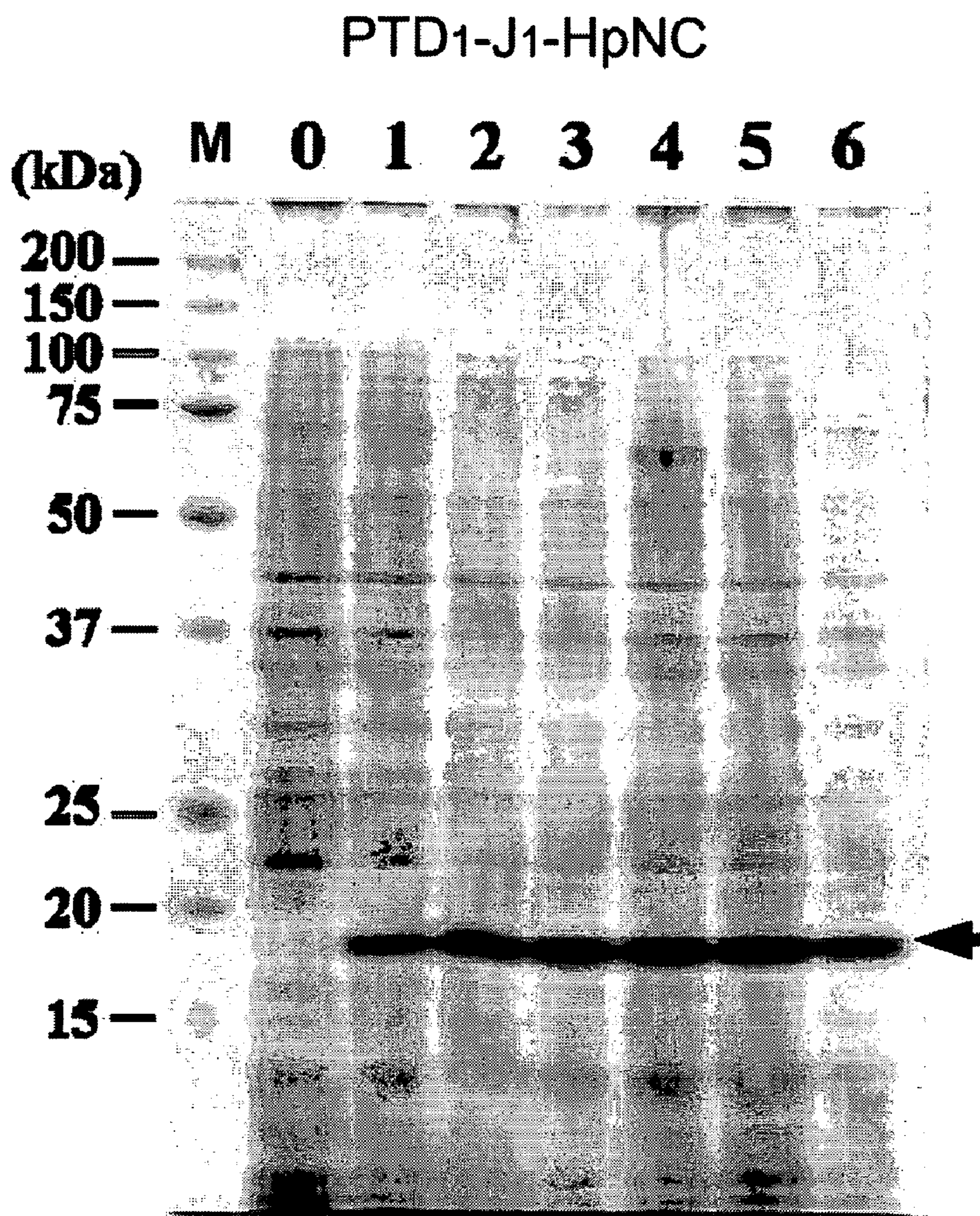


FIG. 10A

IPTG Induction Period (hr)	1	2	3	4	5	6
Recombinant Protein / Total Proteins (% w/w)	26	39	43	38	36	33

FIG. 10B

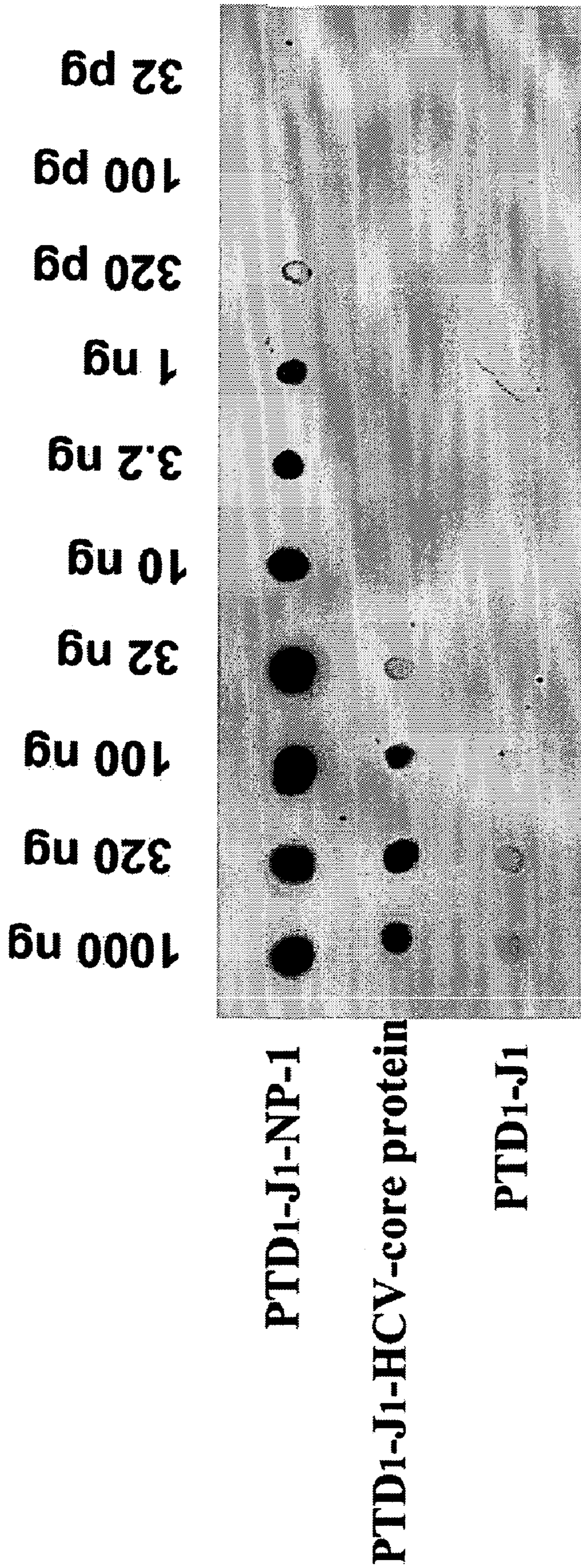


FIG. 11

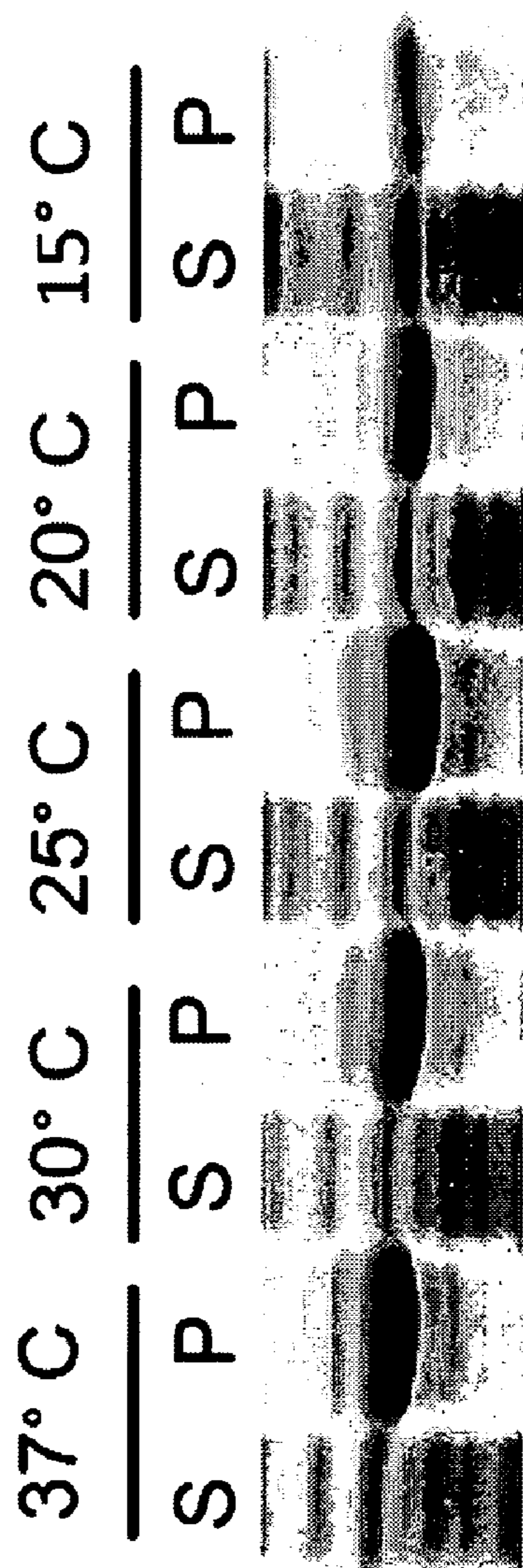


FIG. 12A

Thioredoxin A-
cIGF-I



FIG. 12B

PTD1-J1-cIGF-I

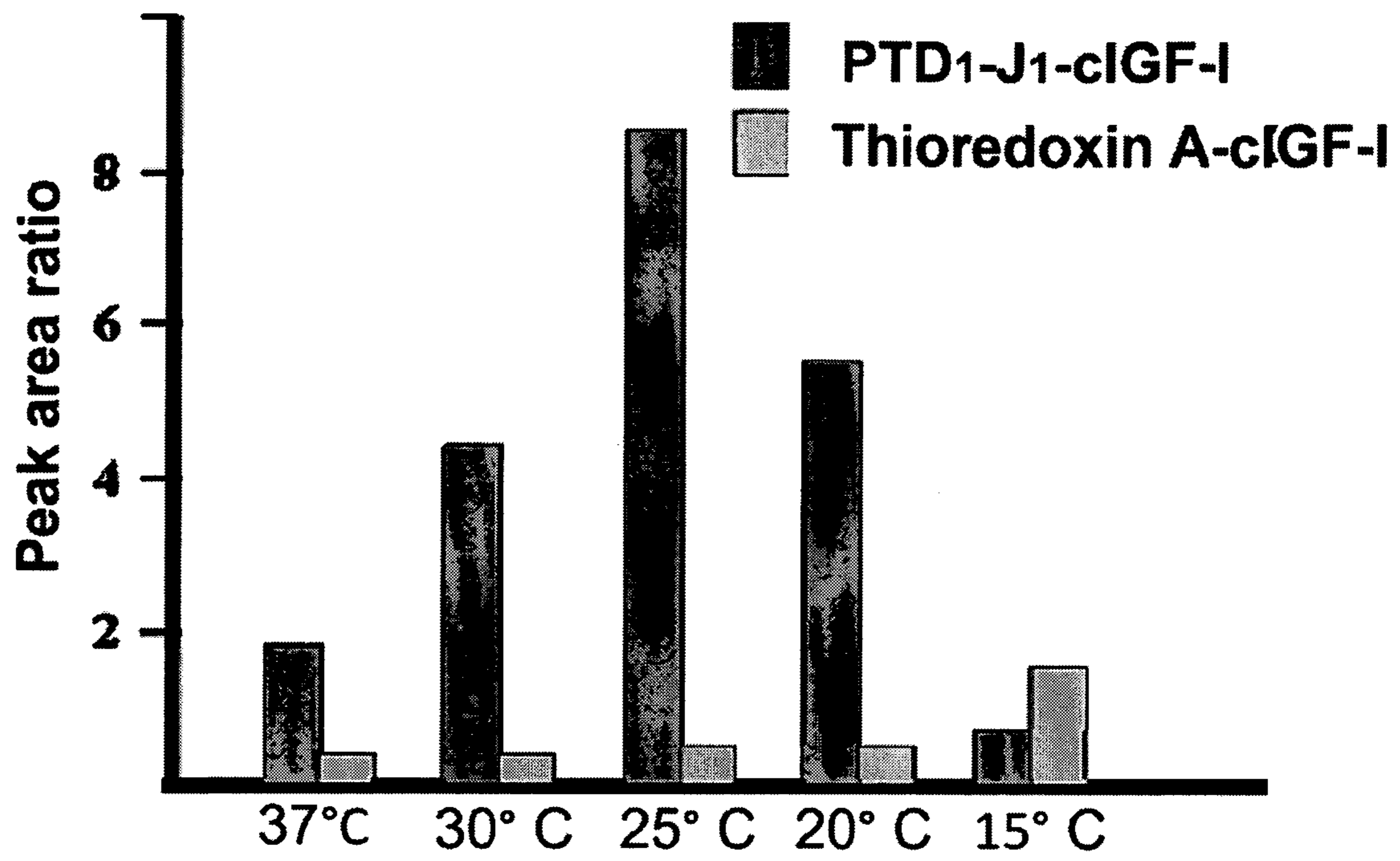


FIG. 13

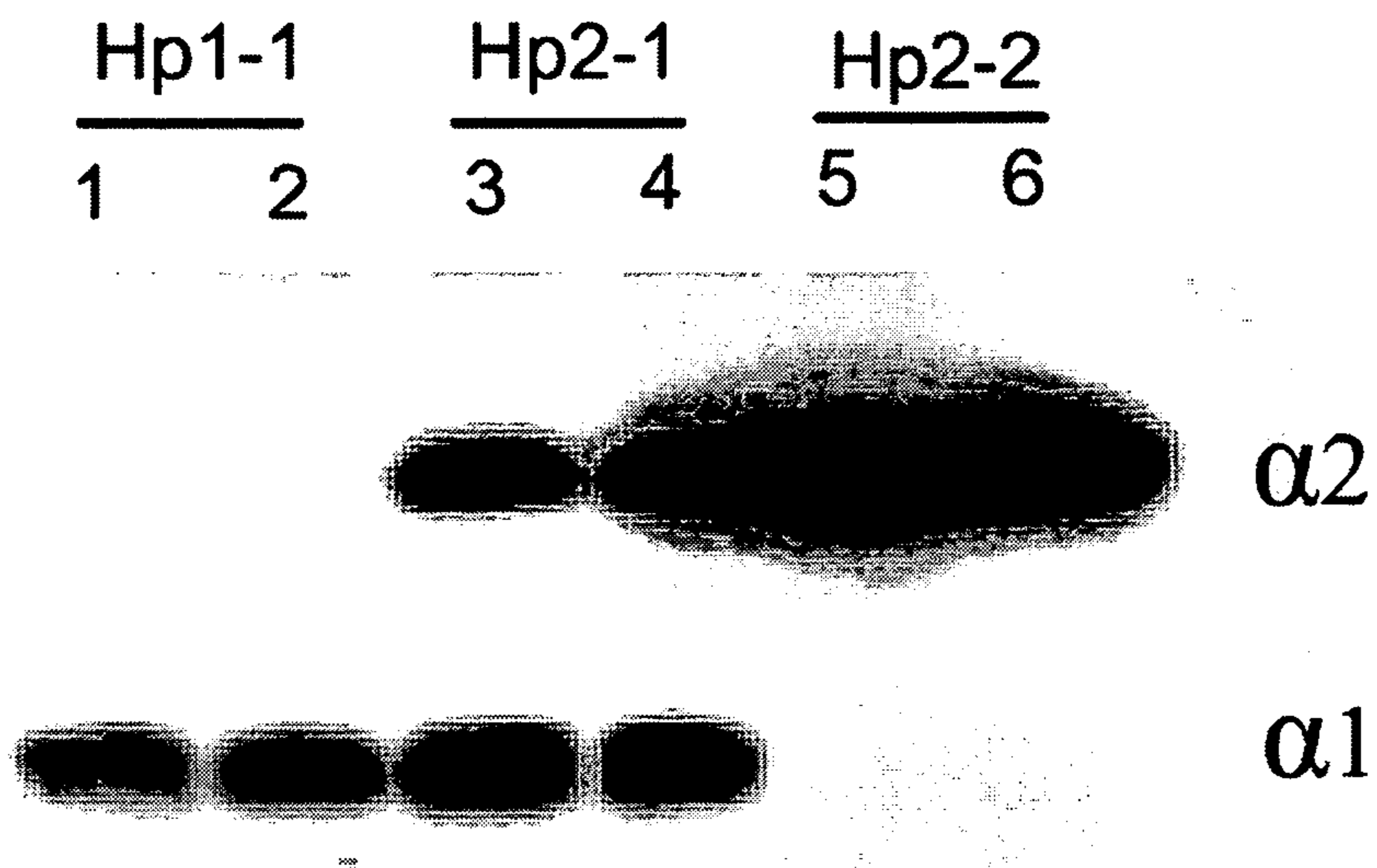


FIG. 14A

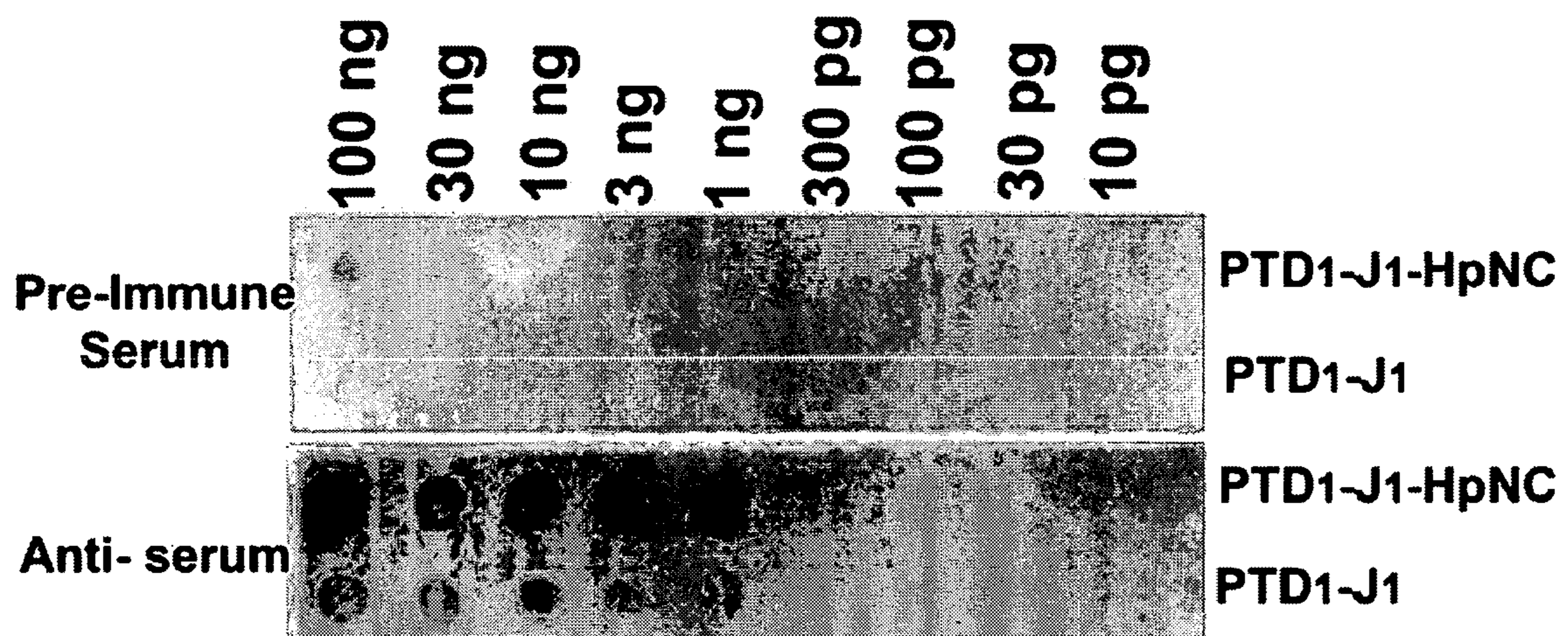


FIG. 14B

EXPRESSION SYSTEM FOR ENHANCING SOLUBILITY AND IMMUNOGENICITY OF RECOMBINANT PROTEINS

REFERENCES TO RELATED APPLICATION

The present application is a Divisional of U.S. application Ser. No. 12/149,606, filed May 5, 2008, now U.S. Pat. No. 7,524,648, and which is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

The present invention relates generally to an expression system and more specifically to an expression system for recombinant proteins with enhanced solubility and immunogenicity.

BACKGROUND OF THE INVENTION

The demand for efficient and large scale production of therapeutic proteins is steadily increasing as more recombinant proteins are approved for use in humans. Using *E. coli* expression system for production of recombinant proteins, however, frequently results in formation of water-insoluble protein inclusion bodies, instead of functional, soluble proteins. Additionally, resolubilized proteins from inclusion bodies do not elicit as strong an immune responses in rats and mice as soluble, native protein does.

The Hsp70-peptide antigen complex plays an important role in the antigen presentation process (Mycko et al., 2004; Bendz et al., 2007). The molecular chaperone/co-chaperone pair (Hsp70/Hsp40) is highly conserved throughout evolution. Eukaryotic Hsp70 genes are descents of the bacterial DnaK gene. DnaK and HSP70 have over 50% homology in their amino acid sequences. The structure of DnaK/Hsp70 is composed of a N-terminal ATPase domain, a substrate binding domain, and a C-terminal lid domain (Genevaux et al., 2007; Shaner & Morano, 2007). Hsp40s represent a large protein family that functions to specify the cellular action of Hsp70 chaperone proteins. There are 44 members of Hsp40 genes found in human genome. Twelve of them are descents of *E. coli* DnaJ. Although their amino acid sequences outside the J-domain are divergent, the 75 amino acid J-domain of the Hsp40 proteins is highly conserved. The J-domain of Hsp40 interacts directly with the Hsp70 ATPase domain to enhance the ATP hydrolysis rate which in turn increases the substrate binding affinity. Hsp40 proteins also bind client substrate and deliver it to the Hsp70 (Fan et al., 2003).

Protein transduction domain (PTD) peptides are able to ferry large molecules into cells independent of classical endocytosis. They are used to enhance cellular uptake of drugs, proteins, polynucleotides and liposomes (Tilstra et al., 2007).

Neither the PTD nor the Hsp40 J-domain has been employed in the development of an expression system for improving solubility and immunogenicity of a recombinant protein. A previously unaddressed need exists in the art to address the aforementioned deficiencies and inadequacies, especially in connection with the development of an expression system for a recombinant protein with enhanced solubility and immunogenicity.

SUMMARY OF THE INVENTION

The invention is related to a protein expression vector for increasing the solubility of a target protein or polypeptide in

a host cell expression system, and/or enhancing the immunogenicity of a target protein or polypeptide. The expression vector of the invention has superior performances in producing high yields of soluble recombinant proteins when compared to other commercially available *E. coli* expression vectors. In addition, the expression vector of the invention is capable of enhancing the immunogenicity of small peptides that by them-selves are weak in inducing antibodies in animals.

One aspect of the invention relates to a chimeric protein that contains three polypeptide fragments: (a) a first polypeptidyl fragment located at the N-terminal end of the chimeric protein that contains a protein transduction domain (PTD) or a fragment thereof having HIV Tat PTD activity; (b) a second polypeptidyl fragment located at the C-terminal end of the first polypeptidyl fragment that contains a J-domain or a fragment thereof having heat shock protein 70 (Hsp70)-interacting activity; and (c) a third polypeptidyl fragment at the C-terminal end of the second polypeptidyl fragment that contains a target protein or polypeptide.

Another aspect of the invention relates to a chimeric gene that includes three DNA sequences: (a) a first DNA sequence encoding a protein transduction domain (PTD) or a fragment thereof having HIV Tat PTD activity; (b) a second DNA sequence encoding, linked in translation frame with the first DNA sequence, encoding a J-domain or a fragment thereof having heat shock protein 70 (Hsp70)-interacting activity; and (c) a third DNA sequence encoding, linked in translation frame with the second DNA sequence, encoding a target protein or polypeptide.

Another aspect of the invention relates to a chimeric gene that comprises two DNA sequences: (a) a first DNA sequence encoding a protein transduction domain (PTD) or a fragment thereof having HIV Tat PTD activity; and (b) a second DNA sequence encoding, linked in translation frame with the first DNA sequence, encoding a J-domain or a fragment thereof having heat shock protein 70 (Hsp70)-interacting activity.

Further another aspect of the invention relates to a protein expression vector that comprises a chimeric gene as aforementioned. Yet another aspect of the invention relates to an isolated host cell that contains an expression vector having chimeric gene as aforementioned.

Another aspect of the invention relates to a method for enhancing immunogenicity and/or solubility of a target protein or polypeptide in a host cell expression system. The method includes the steps of: (a) generating a protein expression vector as aforementioned; (b) transfecting a host cell with the expression vector; (c) culturing the host cell transfected with the expression vector under conditions that permit expression of the target protein or polypeptide; and (d) isolating the target protein or polypeptide.

Further another aspect of the invention relates to a method of expressing a target protein or polypeptide. The method contains the steps of: (a) transfecting a host cell with the expression vector as aforementioned; (b) culturing the host cell transfected with the expression vector under conditions that permit expression of the target protein or polypeptide; and (c) isolating the target protein or polypeptide.

These and other aspects will become apparent from the following description of the preferred embodiment taken in conjunction with the following drawings, although variations and modifications therein may be affected without departing from the spirit and scope of the novel concepts of the disclosure.

The accompanying drawings illustrate one or more embodiments of the invention and, together with the written description, serve to explain the principles of the invention.

Wherever possible, the same reference numbers are used throughout the drawings to refer to the same or like elements of an embodiment.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A-1C illustrate plasmid maps.

FIG. 2A shows the nucleotide sequence and the encoded amino acid sequence of the plasmid of FIG. 1A.

FIG. 2B shows the nucleotide sequence and the encoded amino acid sequence of the plasmid of FIG. 1B.

FIG. 3 is a schematic drawing of the assembly PCR.

FIG. 4A is a photograph of SDS-PAGE gel electrophoresis of the protein samples from *E. coli* whole cell lysates. M stands for protein molecular weight marker, lanes 2-9: protein bands from the whole cell lysates after the indicated induction period; "0" stands for "un-induced." The arrow indicates the protein band of the target recombinant protein, PTD₁-J₁-HSPA1A peptide I.

FIG. 4B is a chart showing the weight percentage of the recombinant protein relative to the total proteins after the various induction periods.

FIG. 5A is a photograph of SDS-PAGE gel electrophoresis of the protein samples from *E. coli* whole cell lysates. M stands for protein molecular weight marker, lanes 2-9: protein bands from the whole cell lysates after the indicated induction period; "0" stands for "un-induced." The arrow indicates the protein band of the target recombinant protein, PTD₁-J₁-HSPA1A peptide II.

FIG. 5B is a chart showing the weight percentage of the recombinant protein relative to the total proteins after the various induction periods.

FIG. 6A is a photograph of SDS-PAGE gel electrophoresis of the protein samples from *E. coli* whole cell lysates. M stands for protein molecular weight marker; lanes 2-9: protein bands from the whole cell lysates after the indicated induction period; "0" stands for "un-induced." The arrow indicates the protein band of the target recombinant protein, PTD₁-J₁-HSPA1A peptide III.

FIG. 6B is a chart showing the weight percentage of the recombinant protein relative to the total proteins after the various induction periods.

FIG. 7A is a photograph of SDS-PAGE gel electrophoresis of the protein samples from *E. coli* whole cell lysates. M stands for protein molecular weight marker, lanes 2-9: protein bands from the whole cell lysates after the indicated induction period; "0" stands for "un-induced." The arrow indicates the protein band of the target recombinant protein, PTD₁-J₁-cIGF-I.

FIG. 7B is a chart showing the weight percentage of the recombinant protein relative to the total proteins after the various induction periods.

FIG. 8A is a photograph of SDS-PAGE gel electrophoresis of the protein samples from *E. coli* whole cell lysates. M stands for protein molecular weight marker; lanes 2-9: protein bands from the whole cell lysates after the indicated induction period; "0" stands for "un-induced." The arrow indicates the protein band of the target recombinant protein, PTD₁-J₁-HA_RBD.

FIG. 8B is a chart showing the weight percentage of the recombinant protein relative to the total proteins after the various induction periods.

FIG. 9A is a photograph of SDS-PAGE gel electrophoresis of the protein samples from *E. coli* whole cell lysates. M stands for protein molecular weight marker, lanes 2-9: protein bands from the whole cell lysates after the indicated induction

period; "0" stands for "un-induced." The arrow indicates the protein band of the target recombinant protein, PTD₁-J₁-HCV-core protein.

FIG. 9B is a chart showing the weight percentage of the recombinant protein relative to the total proteins after the various induction periods.

FIG. 10A is a photograph of SDS-PAGE gel electrophoresis of the protein samples from *E. coli* whole cell lysates. M stands for protein molecular weight marker, lanes 2-9: protein bands from the whole cell lysates after the indicated induction period; "0" stands for "un-induced." The arrow indicates the protein band of the target recombinant protein, PTD₁-J₁-HpNC.

FIG. 10B is a chart showing the weight percentage of the recombinant protein relative to the total proteins after the various induction periods.

FIG. 11 is a photograph showing the result of a Dot blot analysis.

FIG. 12A is a photograph of SDS-PAGE gel electrophoresis. "S" stands for supernatant; "P" stands for insoluble pellet fraction. Prior to being loaded into the gel, the insoluble pellet was dissolved in SDS-PAGE loading buffer.

FIG. 12B is a photograph of SDS-PAGE gel electrophoresis. The labels for lanes 1-10 are the same as FIG. 12A.

FIG. 13 is a chart showing the effects of the temperature on the recombinant protein expression. The peak area ratio represents the relative ratio of the recombinant proteins in the soluble fraction of *E. coli* cell lysate against a constitutively expressed internal protein.

FIG. 14A is a photograph of SDS-PAGE gel electrophoresis.

FIG. 14B is a photograph showing the result of a Dot blot analysis.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

The terms used in this specification generally have their ordinary meanings in the art, within the context of the invention, and in the specific context where each term is used. Certain terms that are used to describe the invention are discussed below, or elsewhere in the specification, to provide additional guidance to the practitioner regarding the description of the invention. For convenience, certain terms may be highlighted, for example using italics and/or quotation marks. The use of highlighting has no influence on the scope and meaning of a term; the scope and meaning of a term is the same, in the same context, whether or not it is highlighted. It will be appreciated that same thing can be said in more than one way. Consequently, alternative language and synonyms may be used for any one or more of the terms discussed herein, nor is any special significance to be placed upon whether or not a term is elaborated or discussed herein. Synonyms for certain terms are provided. A recital of one or more synonyms does not exclude the use of other synonyms. The use of examples anywhere in this specification including examples of any terms discussed herein is illustrative only, and in no way limits the scope and meaning of the invention or of any exemplified term. Likewise, the invention is not limited to various embodiments given in this specification.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. In the case of conflict, the present document, including definitions will control.

As used herein, “around”, “about” or “approximately” shall generally mean within 20 percent, preferably within 10 percent, and more preferably within 5 percent of a given value or range. Numerical quantities given herein are approximate, meaning that the term “around”, “about” or “approximately” can be inferred if not expressly stated.

The term “fusion protein,” also known as “chimeric protein,” refers to “a protein created through the joining of two or more genes which originally coded for separate proteins.”

The term “immunogenicity” refers to the ability of antigen to provoke an immune response.

The term “enhancing solubility of a target protein or polypeptide” refers to “a significant increase in the amount of target protein or polypeptide that otherwise form inclusion bodies is expressed in soluble state when compared to a thioredoxin-fused target protein.

The invention is related to a recombinant protein expression vector that can enhance the immunogenicity of a target protein or polypeptide and increase its solubility in a host cell expression system.

An expression vector system containing a Hsp40 family proteins J-domain was designed to examine whether a target protein expressed using the J-domain-containing expression system of the invention would have an increased solubility when compared to the target protein expressed using other expression systems where insoluble inclusion bodies were formed. In addition, a protein transduction domain (PTD) (11 amino acid residues in length) (Ryu et al., 2003; Jones et al., 2005) of HIV Tat protein was fused to the N-terminus of the J-domain to facilitate the recombinant protein PTD₁J₁-polypeptide to penetrate cell membranes when the fusion polypeptide would be used as an antigen (Wadia et al., 2004; Kaplan et al., 2005). After penetrating the cell membrane of antigen presenting cells (APCs), the J-domain would target to the Hsp70 ATPase domain and thereby allow the fusion polypeptide to be caught by the Hsp70 substrate binding site. The Hsp70-peptide antigen complex has been known to play an important role in the process of antigen presentations.

The invention is related to a recombinant protein expression vector that can enhance the immunogenicity of a target protein or polypeptide, and increase the solubility of a target protein or polypeptide in a host cell expression system. Utilizing the ability of the J-domain of the mammalian Hsp40s in targeting to bacterial DnaK, an *E. coli* expression vector was designed to express recombinant proteins that had been proven forming insoluble inclusion bodies in other expression vectors to investigate whether the J-domain would help folding and thus increased the solubility of the fusion polypeptide/protein. In addition, a protein transduction domain (PTD) (11 amino acid residues in length) (Ryu et al., 2003; Jones et al., 2005) of HIV Tat protein was fused to the N-terminus of the J-domain to facilitate the recombinant protein PTD₁J₁-polypeptide to penetrate cell membranes when the fusion polypeptide would be used as an antigen (Wadia et al., 2004; Kaplan et al., 2005). After penetrating the cell membrane of antigen presenting cells (APCs), the J-domain would target to the Hsp70 ATPase domain and thereby allow the fusion polypeptide to be caught by the Hsp70 substrate binding site. The Hsp70-peptide antigen complex has been known to play an important role in the process of antigen presentations.

One aspect of the invention relates to a chimeric protein that contains three polypeptide fragments: (a) a first polypeptidyl fragment located at the N-terminal end of the fusion protein that contains a protein transduction domain (PTD) or a fragment thereof having HIV Tat PTD activity; (b) a second polypeptidyl fragment located at the C-terminal end of the

first polypeptidyl fragment that contains a J-domain or a fragment thereof having heat shock protein 70 (Hsp70)-interacting activity; and (c) a third polypeptidyl fragment at the C-terminal end of the second polypeptidyl fragment that contains a target protein or a polypeptide. The first polypeptidyl fragment of the chimeric protein may include an amino acid sequence set forth by SEQ ID NO: 1. The second polypeptidyl fragment of the chimeric protein may contain an amino acid sequence set forth by SEQ ID NO: 3.

Another aspect of the invention relates to a chimeric gene that includes three DNA sequences: (a) a first DNA sequence encoding a protein transduction domain (PTD) or a fragment thereof having HIV Tat PTD activity; (b) a second DNA sequence encoding, linked in translation frame with the first DNA sequence, encoding a J-domain or a fragment thereof having heat shock protein 70 (Hsp70)-interacting activity; and (c) a third DNA sequence encoding, linked in translation frame with the second DNA sequence, encoding a target protein or polypeptide.

Another aspect of the invention relates to a chimeric gene that comprises two DNA sequences: (a) a first DNA sequence encoding a protein transduction domain (PTD) or a fragment thereof having HIV Tat PTD activity; and (b) a second DNA sequence encoding, linked in translation frame with the first DNA sequence, encoding a J-domain or a fragment thereof having heat shock protein 70 (Hsp70)-interacting activity.

The J-domain may be at least one selected from the group consisting of a heat shock protein 40 (Hsp40) J-domain and a simian virus 40 (SV40) large T antigen (TAg) J-domain. The SV40 TAg J-domain is located within the N-terminal domain (residues 1 to 82) of SV40 TAg. It has been reported that the N-terminal J-domain of TAg shares functional homology with the Hsp40 J domain (DeCaprio et al., 1997). In one embodiment of the invention, the J-domain is a human heat shock protein 40 J-domain.

The first DNA sequence of the chimeric gene may encode a protein transduction domain (PTD) that contains an amino acid sequence set forth by SEQ ID NO: 1. The second DNA sequence of the chimeric gene may encode a J-domain comprising an amino acid sequence set forth by SEQ ID NO: 3.

Another aspect of the invention relates to a method for enhancing immunogenicity and/or solubility of a target protein or polypeptide in a host cell expression system. The method includes the steps of: (a) generating a protein expression vector as aforementioned; (b) transfecting a host cell with the expression vector; (c) culturing the host cell transfected with the expression vector under conditions that permit expression of the target protein or polypeptide; and (d) isolating the target protein or polypeptide.

Further another aspect of the invention relates to a method of expressing a target protein or polypeptide. The method contains the steps of: (a) transfecting a host cell with the expression vector as aforementioned; (b) culturing the host cell transfected with the expression vector under conditions that permit expression of the target protein or polypeptide; and (c) isolating the target protein or polypeptide.

Further another aspect of the invention relates to a protein expression vector that comprises one of the aforementioned chimeric genes.

Yet another aspect of the invention relates to an isolated host cell that contains an expression vector having one of the aforementioned chimeric genes.

EXAMPLES

Without intent to limit the scope of the invention, exemplary instruments, apparatus, methods and their related

results according to the embodiments of the present invention are given below. Note that titles or subtitles may be used in the examples for convenience of a reader, which should in no way limit the scope of the invention. Theories are proposed and disclosed herein should in no way limit the scope of the invention so long as the invention is practiced according to the invention without regard for any particular theory or scheme of action.

Example 1

Construction of pET22b-PTD₁-J₁ Expression Vector

FIGS. 1A-1C illustrate three pET22b derivatives plasmids: pET22b-PTD₁, pET22b-PTD₁-J₁, and pET22b-PTD₁-J₁-target protein (or antigenic protein). These plasmids were generated using the methods as described below.

Plasmid pET22b-PTD₁. The plasmid pET22b-PTD₁ contains a HIV tat PTD₁ (native form) gene insert between the restriction enzymes NdeI and BamHI, as shown in FIG. 2A. The PTD₁ gene, which encodes the amino acid sequence of PTD₁ (SEQ ID NO: 1), was synthesized using the oligonucleotide pair, PTD₁ f (TATGTATGGTTCGTAAGAACGTCGT-CAGCGTCGTCGTGG; SEQ ID NO: 5) and PTD₁ r (GATC-CCACGACGACGCTGACGACGTTTCTTACGACCATACA; SEQ ID NO: 6). The oligonucleotide pair encoding the optimized codons of protein transduction domain (PTD₁) (SEQ ID NO: 1) for *E. coli* were phosphorylated by polynucleotide kinase before annealing to the double strand form in order to be inserted into the pET22b vector (Novagen, Madison, Wis.) to generate pET22b-PTD₁ (FIG. 1A). Before ligating with the PTD₁ gene insert, the pET22b vector was co-digested by NdeI and BamHI and dephosphorylated by calf intestine alkaline phosphatase (CIAP). FIG. 2A shows the detailed nucleotide sequence of the plasmid pET22b-PTD₁ and encoded PTD₁ amino acid sequence.

Plasmid pET22b-PTD₁-J₁. The plasmid pET22b-PTD₁-J₁ contains a fusion gene with the PTD₁ gene being fused to the N-terminus of the HSP40 J domain gene. The fusion gene encodes a chimeric protein PTD₁-J₁. The J domain of the HSP40 gene was synthesized by assembly PCR using the oligonucleotides that were designed to obtain optimized codons for *E. coli*. Table 1 lists the nucleotide sequences of the oligonucleotide primers (SEQ ID NOs: 7 to 16) used in the assembly PCR synthesis of the HSP40 J domain. The concentrations of the primers in the assembly PCR reaction mixture were adjusted as follows: 0.5 μM of F1 and R1 and 0.05 μM of F2, F3, R3, and R2, and so on in the reaction mixture. The assembly PCR profile was 2 min at 94° C., 20 sec at 94° C., 40 sec at 40° C., 20 sec at 72° C. of 20 cycles, and 5 min at 72° C.

The PCR product was cloned into pGEM-T Easy vector (Promega) for colony selection and DNA sequencing. The plasmid with correct DNA sequence encoding Hsp40-J domain (SEQ ID NO: 3) was co-digested by BamHI and EcoRI to remove the 0.2 kb inserted DNA fragment from pGEM-T Easy vector. This DNA fragment was then inserted into pET22b-PTD₁ vector, which had been digested by BamHI/EcoRI and CIAP, to generate the pET22b-PTD₁-J₁ expression vector (FIG. 1B). FIG. 2B shows the detailed nucleotide sequence of the plasmid pET22b-PTD₁-J₁ and the amino acid sequence of the encoded fusion protein PTD₁-J₁. FIG. 3 is a schematic drawing of the assembly PCR, which is an artificial synthesis of long DNA sequences by performing PCR on a pool of long oligonucleotides with short overlapping segments.

TABLE 1

Primer Sequence	Sequence ID
J1 tggatcctgggtaagattactaccagactc nBF1 acggtctc	SEQ ID NO: 7
F2 tactaccagactcacggtctcgctcgtgggtg catctgatgatgaaatc	SEQ ID NO: 8
F3 ggtgcatctgatgatgaaatcaaactgctt accgctcgcaggcactg	SEQ ID NO: 9
F4 gttaccgctcgtcaggcactgcggttaccatc cagacaaaaacaaagaa	SEQ ID NO: 10
F5 taccatccagacaaaaacaaagaaccgggtg cagaagagaaattc	SEQ ID NO: 11
F6 cggggtgcagaagagaaattcaaagatcg cagaagcatacgacgtt	SEQ ID NO: 12
EcoRI cgaattcgcaccaccagaaccacctttcaga R1 ccttc	SEQ ID NO: 13
R2 agaaccacctttcagacctttcttcaccgtaa cggtcgaagatttcacg	SEQ ID NO: 14
R3 gtaacggtcgaagattttcagctttacgtgga tcgctcagaacgtcgtta	SEQ ID NO: 15
R4 tggatcgctcagaacgtcgtatgcttctgctg atctc	SEQ ID NO: 16

Plasmid pET22b-PTD₁-J₁-Target protein. The plasmid pET22b-PTD₁-J₁-target protein contains a fusion gene encoding a chimeric protein, PTD₁-J₁-target protein. Target proteins that were inserted into the expression vector pET22b-PTD₁-J₁ included those proteins that had been proven to form insoluble inclusion bodies due to the solubility issue when using other expression vectors, and small peptides that are weak in inducing immunogenicity and/or having solubility issues in *E. coli* expression system. A DNA fragment comprising a codon-optimized cDNA sequence encoding a target protein to be expressed in the pET22b-PTD₁-J₁ expression vector was synthesized by PCR, and the PCR product was then inserted into the pET22b-PTD₁-J₁ vector at EcoRI and XhoI sites to generate the plasmid pET22b-PTD₁-J₁-target protein. The resulting plasmid was transformed into *E. coli* Rosetta (Novagen) competent cells to obtain clones.

Example 2

Expression and Analyses of Recombinant Proteins

Chimeric proteins, PTD₁-J₁-target protein, were expressed in *E. coli* cultures containing corresponding expression plasmids. In brief, the colony resistant to ampicillin and chloramphenicol was cultured and amplified in TYD medium (10 g trypton, 20 g yeast extract, 5 g NaCl, 2 g Dextrose per liter, pH 7.2). Once OD₆₀₀ reached 0.3±0.1, the bacterial culture was induced with isopropylthio-β-D-galactoside (IPTG; Promega, USA) at a final concentration of 1 mM at 37° C. in a rotating incubator shaken at 225 rpm. After the IPTG induction, the cells were collected by centrifugation at 5,000×g for 10 min, washed once with PBS, resuspended in PBS and homogenized by sonication. The sonicated lysates were centrifuged at 15,000×g for 30 min. Twenty microliters of total lysates from 0.3 OD₆₀₀ unit of *E. coli* cells were mixed with 30 μL of 2×SDS-PAGE loading buffer, and the mixture was loaded into each well of the gel. The protein bands were visualized by Coomassie brilliant blue R250 staining of the

gel, and scanned by laser densitometer (Personal Densitometer SI, Molecular Dynamics). The amount of each recombinant protein over the amount of total protein was calculated and represented as percentage weight.

Example 3

Expression of Human HSPA1A Peptide I

A DNA fragment comprising a codon-optimized cDNA sequence (SEQ ID NO: 17) encoding the amino acid sequence (SEQ ID NO: 18) of human heat shock 70 kDa protein 1A (HSPA1A) Peptide I was synthesized by assembly PCR using the primers listed in Table 2. The assembly PCR profile was 2 min at 94° C., 20 sec at 94° C., 40 sec at 40° C., 20 sec at 72° C. of 20 cycles, and 5 min at 72° C. The PCR product was then inserted in the expression vector pET22b-PTD₁-J₁ to generate the plasmid pET22b-PTD₁-J₁-HSPA1A peptide I using the method described in Example 1.

TABLE 2

Primer	Sequence	Sequence ID
RI-I-f1	gaattctagcagcagcaccagggcgagcc tggaaattgatagcctgttt	SEQ ID NO: 19
I-f2	agcctggaaattgatagcctgtttgaagg cattgat tttataaccagc	SEQ ID NO: 20
I-f3	gtttgaaggcattgatttttataaccagca tt acccgtgcgcgttttgaa	SEQ ID NO: 21
I-r3	gggtgctacgaaacagatcgctgcacagt tcttcaaaacgcgcacgggt	SEQ ID NO: 22
I-r2	catcagcagcgcgtttttccaccgggtcc aggggtgctacgaaacagatc	SEQ ID NO: 23
Xho-I-r1	ctcgagaatctgcgctttatccagtttcg catc acgcagcgtttttc	SEQ ID NO: 24

Plasmid pET22b-PTD₁-J₁-HSPA1A peptide I that carried the genes encoding the recombinant protein PTD₁-J₁-HSPA1A peptide I was transformed into *E. coli* Rosetta. The recombinant protein expression was induced by IPTG according to the method described above for up to 16 hours and the amounts of protein induced in the cell extract determined as in Example 2.

FIG. 4A shows a Coomassie® blue stained SDS-PAGE gel analysis of *E. coli* whole cell lysates. The protein bands shown between 15 kDa and 20 kDa (indicated by an arrow) correspond to the target protein, pET22b-PTD₁-J₁-HSPA1A peptide I. Lane 1: standard molecular weight marker. Lanes 2-9: whole cell lysates after the IPTG induction, where “0 hr” stands for “uninduced.”

The effect of induction period of IPTG induction on the yield of the PTD₁-J₁-HSPA1A peptide I expression was quantitated and represented by the weight percentage of the recombinant PTD₁-J₁-HSPA1A peptide I over the total proteins. As shown in FIG. 4B, the induction reached a plateau after about 4 hrs. The expression of PTD₁-J₁-HSPA1A peptide I declined as the IPTG induction was extended to 16 hours.

Example 4

Expression of human HSPA1A Peptide II

A DNA fragment comprising a codon-optimized cDNA sequence (SEQ ID NO: 25) encoding the amino acid

sequence (SEQ ID NO: 26) of human heat shock 70 kDa protein 1A (HSPA1A) peptide II was synthesized by assembly PCR using the primers (SEQ ID NO: 27 to SEQ ID NO: 33) listed in Table 3. The assembly PCR profile was 2 min at 94° C., 20 sec at 94° C., 40 sec at 40° C., 20 sec at 72° C. of 20 cycles, and 5 min at 72° C. The PCR product was then inserted in the expression vector pET22b-PTD₁-J₁ to generate the plasmid pET22b-PTD₁-J₁-HSPA1A peptide II using the method described in Example 1.

TABLE 3

Primer	Sequence	Sequence ID
RI-II-f1	gaattctaaccgtaaccgctactgacaa atccactggtaaagctaacaag	SEQ ID NO: 27
II-f2	tccactggtaaagctaacaagatcacc atcaccaacgacaaaggtcgtc	SEQ ID NO: 28
II-g3	atcaccaacgacaaaggtcgctctgtcc aaggaagagatcgagcgtatgg	SEQ ID NO: 29
II-f4	aaggaagagatcgagcgtatggttcag gaagctgaaaagtacaag	SEQ ID NO: 30
II-r3	acgctgaacttcgtcttcagccttgta cttttcagcttctctgaacc	SEQ ID NO: 31
II-r2	agcgttcttagcggaaacacggttcacg ctgaacttcgtcttcagc	SEQ ID NO: 32
Xho-II-r1	ctcgaggaaagcgtaggattccagagc gttcttagcggaaacagttca	SEQ ID NO: 33

Plasmid pET22b-PTD₁-J₁-HSPA1A peptide II that carried the genes encoding the recombinant protein PTD₁-J₁-HSPA1A peptide II was transformed into *E. coli* Rosetta. The recombinant protein expression was induced by IPTG according to the method described above. The amount of protein induced in the cell lysate over the 16 hours IPTG induction was monitored as in Example 2 above.

FIG. 5A shows a Coomassie® blue stained SDS-PAGE gel analysis of *E. coli* whole cell lysates. The protein bands shown between 15 kDa and 20 kDa (indicated by an arrow) correspond to the chimera protein PTD₁-J₁-HSPA1A peptide II. Lane 1: standard molecular weight marker. Lanes 2-9: whole cell lysates after the IPTG induction, where “0 hr” stands for “uninduced.”

The amount of the PTD₁-J₁-HSPA1A peptide II expression after each induction period was quantitated and the yield expressed as the weight percentage of the recombinant PTD₁-J₁-HSPA1A peptide II over the total proteins. As shown in FIG. 5B, the induction reached a plateau after 4 hrs. The expression of PTD₁-J₁-HSPA1A peptide II declined as the IPTG induction was extended to 16 hours.

Example 5

Expression of Human HSPA1A Peptide III

A DNA fragment comprising a codon-optimized cDNA sequence (SEQ ID NO: 34) encoding the amino acid sequence (SEQ ID NO: 35) of human heat shock 70 kDa protein 1A (HSPA1A) peptide III was synthesized by assembly PCR using the primers (SEQ ID NO: 36 to SEQ ID NO: 42) listed in Table 4. The assembly PCR profile was 2 min at 94° C., 20 sec at 94° C., 40 sec at 40° C., 20 sec at 72° C. of 20 cycles, and 5 min at 72° C. The PCR product was then inserted in the expression vector pET22b-PTD₁-J₁ to gener-

ate the plasmid pET22b-PTD₁-J-HSPA1A peptide III using the method described in Example 1.

TABLE 4

Primer	Sequence	Sequence ID
RI-III-f1	gaattctgaagatgaaggcctgaaag gcaaaaattagcgaagcggat	SEQ ID NO: 36
III-f2	ggcaaaattagcgaagcggataagaa aaaggtgctg gataaatgccag	SEQ ID NO: 37
III-f3	ggtgctggataaatgccag gaagtg attagctggctg gatgcgaacacc	SEQ ID NO: 38
III-f4	gctggatgcgaacacctggcggaaa aagatgaattt gaacataaacgt	SEQ ID NO: 39
III-r3	ttccagttctttacgtttatgttcaa atcatctttttccgccag	SEQ ID NO: 40
III-r2	cgggttgcacacctgttccagttctt tagtttatgttcaaattcatc	SEQ ID NO: 41
Xho-III-r1	ctggagcgcgcctgatacagccgc taataatcgggttgcacacctg	SEQ ID NO: 42

Plasmid pET22b-PTD₁-J₁-HSPA1A peptide III that carried the genes encoding the recombinant protein PTD₁-J₁-HSPA1A peptide III was transformed into *E. coli* Rosetta. The recombinant protein expression was induced by IPTG according to the method described above. The amount of protein induced in the cell lysate was monitored over the 16 hours IPTG induction as in Example 2 above.

FIG. 6A shows a Coomassie® blue stained SDS-PAGE gel analysis of *E. coli* whole cell lysates. The protein bands shown between 15 kDa and 20 kDa (indicated by an arrow) correspond to the chimera protein PTD₁-J₁-HSPA1A peptide III. Lane 1: standard molecular weight marker. Lanes 2-9: whole cell lysates after the IPTG induction, where “0 hr” stands for “uninduced.”

The amount of the PTD₁-J₁-HSPA1A peptide III expression after each induction period was quantitated and the yield represented by the weight percentage of the recombinant PTD₁-J₁-HSPA1A peptide III over the total proteins. As shown in FIG. 6B, the induction reached a plateau after 2 hrs. The expression of PTD₁-J₁-HSPA1A peptide III declined as the IPTG induction was extended.

Example 6

Expression of Chicken IGF-I

A DNA fragment comprising a codon-optimized cDNA sequence (SEQ ID NO: 43) encoding the amino acid sequence (SEQ ID NO: 44) of chicken IGF-I peptide (cIGF-I) was synthesized by assembly PCR using the primers (SEQ ID NO: 45 to SEQ ID NO: 51) listed in Table 5. The assembly PCR profile was 2 min at 94° C., 20 sec at 94° C., 40 sec at 40° C., 20 sec at 72° C. of 20 cycles, and 5 min at 72° C. The PCR product was then inserted in the expression vector pET22b-PTD₁-J₁ to generate the plasmid pET22b-PTD₁-J₁-cIGF-I using the method described in Example 1.

TABLE 5

Primer	Sequence	Sequence ID
RI-F1	gaattctggtccagaaacctgtgtggtgca	SEQ ID NO: 45
new	gaactggtgatgcactgcagttcgtg	

TABLE 5-continued

Primer	Sequence	Sequence ID
F2	gaactggtgatgcactgcagttcgtgtgtg gtgatcgtggtttctac	SEQ ID NO: 46
F3	ggtgatcgtggtttctacttcagcaaaccga ctggttatggttagctctagc	SEQ ID NO: 47
F4	ggttatggttagctctagccgctcgtctgcac acaaaggtattgtggatg	SEQ ID NO: 48
F5	cacaaaggtattgtggatgaatggtgctttc agagctgtgatctgcgtcg	SEQ ID NO: 49
R2	gattggtgcacagtacatttccagacgacgc agatcacagctctg	SEQ ID NO: 50
Xho-R1	ctcgagtgcgcttttccggtggutgattggtg cacagtacatttcc	SEQ ID NO: 51

Plasmid pET22b-PTD₁-J₁-cIGF-I that carried the genes encoding the recombinant protein PTD₁-J₁-cIGF-I was transformed into *E. coli* Rosetta. The recombinant protein expression was induced by IPTG according to the method described above for up to 6 hours and the amounts of proteins induced in the cell extracts determined as in Example 2 above.

FIG. 7A shows a Coomassie® blue stained SDS-PAGE gel analysis of *E. coli* whole cell lysates. The protein bands shown around 20 kDa (indicated by an arrow) correspond to the chimera protein PTD₁-J₁-cIGF-I. Lane 1: standard molecular weight marker (M). Lanes 2-8: whole cell lysates after the IPTG induction, where “0 hr” stands for “uninduced.” The amount of the PTD₁-J₁-cIGF-I expression after each induction period was quantitated and the yield represented by the weight percentage of the recombinant protein PTD₁-J₁-cIGF-I over the total proteins. As shown in FIG. 7B, the induction reached a plateau after about 2 to 4 hrs.

Example 7

Expression of Avian Influenza Virus HA (H5) Receptor Binding Domain (RBD)

A DNA fragment, which comprises a native viral cDNA sequence (SEQ ID NO: 52) encoding the amino acid sequence (SEQ ID NO: 53) of the receptor binding domain (RBD) of avian Influenza virus Hemagglutinin (HA) subtype H5, was synthesized by PCR using the primer pair (SEQ ID NOs: 54 and 55) listed in Table 6, and avian influenza virus hemagglutinin (HA) subtype H5 cDNA as a DNA template (GeneBank accession number: EF419243). The PCR profile was 2 min at 94° C., 20 sec at 94° C., 40 sec at 60° C., 20 sec at 72° C. of 20 cycles, and 5 min at 72° C. The PCR product was inserted in the expression vector pET22b-PTD₁-J₁ to generate the plasmid pET22b-PTD₁-J₁-HA_RBD using the method described in Example 1 above.

TABLE 6

Primer	Sequence	Sequence ID
RI HA-RBD f	tgaattcgaaacacctattgagca gaataaac	SEQ ID NO: 54
Xho HA-RBD r	tctcgagaattggtgagtcacctt tcttgac	SEQ ID NO: 55

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Plasmid pET22b-PTD₁-J₁-HA_RBD that carried the genes encoding the recombinant protein PTD₁-J₁-HA_RBD was transformed into *E. coli* Rosetta. The recombinant protein expression was induced by IPTG according to the method described above. The amount of protein induced in the cell lysate was monitored over the 16 hours IPTG induction as in Example 2 above.

FIG. 8A shows a Coomassie® blue stained SDS-PAGE gel analysis of *E. coli* whole cell lysates. The protein bands shown between around 37 kDa and 25 kDa (indicated by an arrow) correspond to the chimera protein PTD₁-J₁-HA_RBD. Lane 1: standard molecular weight marker (M). Lanes 2-10: whole cell lysates after the IPTG induction, where “0 hr” stands for “uninduced.” The amount of the PTD₁-J₁-HA_RBD expression after each induction period was quantitated and the yield represented by the weight percentage of the recombinant protein PTD₁-J₁-HA_RBD over the total proteins. As shown in FIG. 8B, the induction reached a plateau after about 3 hrs.

Example 8

Expression of Hepatitis C Virus Core Protein

A DNA fragment, which comprises a native viral cDNA sequence (SEQ ID NO: 56) encoding the amino acid sequence (SEQ ID NO: 57) of the hepatitis C virus (HCV) core protein, was synthesized by PCR using the primer pair (SEQ ID NOs: 58 and 59) listed in Table 7 and a HCV cDNA that was reversely transcribed from a serum sample of an acute, hepatitis C infected-patient as a DNA template. The PCR profile was 2 min at 94° C., 20 sec at 94° C., 40 sec at 60° C., 20 sec at 72° C. of 40 cycles, and 5 min at 72° C. The PCR product was inserted in the expression vector pET22b-PTD₁-J₁ to generate the plasmid pET22b-PTD₁-J₁-HCV-core protein using the method described in Example 1 above.

TABLE 7

Primer	Sequence	Sequence ID
RI-Core f	tgaattcgatgagcacaatacctaaa cctc	SEQ ID NO: 58
Xho-Core r	tctcgagagcagagaccggaacggtg at	SEQ ID NO: 59

Plasmid pET22b-PTD₁-J₁-HCV-core protein that carried the genes encoding the recombinant protein PTD₁-J₁-HCV-core protein was transformed into *E. coli* Rosetta. The recombinant protein expression was induced by IPTG according to the method described above. The amount of protein induced in the cell lysate was monitored over the 16 hours IPTG induction as in Example 2 above.

FIG. 9A shows a Coomassie® blue stained SDS-PAGE gel analysis of *E. coli* whole cell lysates. The protein bands shown between around 37 kDa and 25 kDa (indicated by an arrow) correspond to the chimera protein PTD₁-J₁-HCV-core protein. Lane 1: standard molecular weight marker (M). Lanes 2-8: whole cell lysates after the IPTG induction, where “0 hr” stands for “uninduced.” The amount of the PTD₁-J₁-HCV core protein expression after each induction period was quantitated and the yield represented by the weight percentage of the recombinant protein PTD₁-J₁-HCV core protein

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over the total proteins. As shown in FIG. 9B, the induction reached a plateau after about 5 to 6 hrs.

Example 9

Expression of Human Haptoglobin Fusion Polypeptide

A fusion gene comprising a nucleotide sequence (SEQ ID NO: 60) that encoded an amino acid sequence (SEQ ID NO: 61) of haptoglobin α -chain fusion polypeptide, HpNC, was synthesized by assembly PCR using the primers (SEQ ID NO: 62 to SEQ ID NO: 65) listed in Table 8. The fusion polypeptide HpNC comprises a peptide fragment from the N-terminal portion (DSGNDVTDIADDG, the amino acid residues 1 to 13 of SEQ ID NO: 61) of the mature haptoglobin, a linker (-GSGG-), and a peptide fragment from the C-terminal portion (RHYEGSTVPEKKTPKS, the amino acid residues 18 to 33 of SEQ ID NO: 61) of the premature haptoglobin α -chain. The assembly PCR profile was 2 min at 94° C., 20 sec at 94° C., 40 sec at 40° C., 20 sec at 72° C. of 20 cycles, and 5 min at 72° C. The PCR product was inserted in the expression vector pET22b-PTD₁-J₁ to generate the plasmid pET22b-PTD₁-J₁-HpNC using the method described in Example 1.

Plasmid pET22b-PTD₁-J₁-HpNC that carried the genes encoding the recombinant protein PTD₁-J₁-HpNC was transformed into *E. coli* Rosetta. The recombinant protein expression was induced by IPTG according to the method described above for up to 6 hours, and the amounts of proteins in cell extracts determined as in Example 2.

TABLE 8

Primer Sequence	Sequence ID
RI-F1 agaattctgatagcggcaacgatgtgaccga tattgcgatgatggtgg	SEQ ID NO: 62
F2 tgaccgatattgcgatgatggtgtagtgg tggctcgtcattat	SEQ ID NO: 63
F3 atggtgtagtggtggtcgtcattatgaagg tagcaccgtt	SEQ ID NO: 64
R2 ggttttcttctccggaacggtgctaccttca taatgacgaccaccac	SEQ ID NO: 65
Xho-R1 tctcgagaccaccgctctttggggttttctt ctccggaacggtgcta	SEQ ID NO: 66

FIG. 10A shows a Coomassie® blue stained SDS-PAGE gel analysis of *E. coli* whole cell lysates. The protein bands shown between around 15 kDa and 20 kDa (indicated by an arrow) correspond to the fusion polypeptide PTD₁-J₁-HpNC. Lane 1: standard molecular weight marker (M). Lanes 2-10: total whole cell lysates after the IPTG induction, where “0 hr” stands for “uninduced.” The amount of the PTD₁-J₁-HpNC expression after each induction period was quantitated and the yield expressed as the weight percentage of the recombinant protein PTD₁-J₁-HpNC over the total proteins. As shown in FIG. 10B, the induction reached a plateau after about 3 hrs.

Example 10

Expression of Neutrophil Peptide-1

A cDNA clone comprising a nucleotide sequence (SEQ ID NO: 67) that encodes an amino acid sequence (SEQ ID NO: 68) of Neutrophil peptide-1 (NP-1) was obtained by screen-

ing a rabbit intestine cDNA library. The cDNA fragment was inserted into the expression vector pET22b-PTD₁-J₁ to generate the plasmid pET22b-PTD₁-J₁-NP-1. Plasmid pET22b-PTD₁-J₁-NP-1 that carried the genes encoding the recombinant protein PTD₁-J₁-NP-1 was transformed into *E. coli* Rosetta. The recombinant protein expression was induced by IPTG according to the method described above.

Example 11

Target Protein-Specific Immunogenicity

Immunization of animals. Balb/c Mice of 5-week-old were immunized subcutaneously with 50 µg of the recombinant protein PTD₁-J₁-NP-1 emulsified in TiterMAX Gold adjuvant. Boosts were carried out every 2 weeks. Five days after the second boost, the sera of the mice were collected and assayed for the antibody against the recombinant protein PTD₁-J₁-NP-1. The specificity of anti-serum against NP-1 was determined using the dot blotting assay.

Dot Blotting Assay. Solutions containing various amounts of recombinant proteins (antigens), PTD₁-J-NP-1, PTD₁-J-HCV-core protein, and PTD₁-J₁, were respectively spotted onto PVDF membranes. The membranes were blocked by 5% skim milk in TBSN (25 mM Tris-HCl, pH 7.4, 150 mM NaCl, 0.02% Tween 20) for 1 hour. After 4 washes with TBSN, the membranes were incubated with mouse anti-serum overnight at a dilution 1:1000, unbound primary antibodies (Ab) removed from the membrane by 4 washes with TBSN, and incubated with HRP-conjugated goat anti-mouse secondary Ab (2000× dilution) for 4 hours. The labeled proteins on washed membrane were detected by chemiluminescence according to manufacturer's instructions (Pierce).

As shown in FIG. 11, the mouse anti-serum, at 1000× dilution, was highly sensitive in detecting the antigen PTD₁-J₁-NP-1, less sensitive to PTD₁-J₁-HCV-core protein, and even less sensitive to PTD₁-J₁. The antigen PTD₁-J₁-NP-1 in amounts as small as 320 pg was detectable by the mouse anti-serum (1000× dilution). On the other hand, at least 32 ng of PTD₁-J₁-HCV-core protein was needed to produce an equivalently weak signal. The signal produced by interacting with PTD₁-J₁ was very weak even at the amounts as high as 100 ng. This indicates that more than 99% of anti-serum interacted with the target protein NP-1, and less than 1% interacted with PTD₁-J₁-HCV-core protein and PTD₁-J₁. Therefore, the recombinant protein PTD₁-J₁-NP-1 was able to raise a high titer of antibody specific against the target protein NP-1.

Example 12

Enhanced Solubility of Recombinant Protein

Construction of pET32b-cIGF-I. To compare the solubility of a target protein with the protein fused to a J domain, the construct pET32b-cIGF-I was generated by inserting the EcoRI/XhoI DNA fragment of pET22b-PTD₁-J₁-cIGF-I into the same restriction enzyme sites of pET32b to form a pET32b-cIGF-I expression vector.

Expression of Target Protein. Recombinant proteins were expressed in *E. coli* cultures containing corresponding expression plasmids. In brief, the colony resistant to ampicillin and chloramphenicol was cultured and amplified in TYD medium (10 g trypton, 20 g yeast extract, 5 g NaCl, 2 g Dextrose per liter, pH 7.2) at 37° C. Once the bacterial density reached 0.3±0.1 OD₆₀₀, the incubation temperature of bacterial cultures were set at 37° C., 30° C., 25° C., 20° C. and 15°

C., respectively, and then isopropylthio-β-D-galactoside (IPTG; Promega, USA) was added into the cultures at a final concentration of 1 mM, and induced protein expression for 3, 4, 5, 6 hrs, and overnight, respectively, in a rotating incubator shaken at 225 rpm. After the IPTG induction, the cells were collected by centrifugation at 5,000×g for 10 min, washed once with PBS and resuspended in PBS for homogenization by sonication. The sonicated lysates were centrifuged at 15,000×g for 30 min. Supernatants (soluble fractions) were collected. The pellets (insoluble fractions) were washed once with PBS to remove residual soluble proteins before re-suspending in PBS to obtain the insoluble fractions, which included protein inclusion bodies. About 30 µl of each fraction from the amount equivalent of 0.5 OD₆₀₀ unit of *E. coli* cells were loaded into each well of the gel. The gel was stained with Coomassie brilliant blue R-250 and scanned by laser densitometer (Personal Densitometer SI, Molecular Dynamics).

Results:

Expression of thioredoxin fusion protein of cIGF-I. The mature cIGF-I polypeptide (70 amino acid residues) contains 6 cysteines that make 3 disulfide bonds. This protein is very difficult to be expressed in *E. coli* in a soluble form. The pET32-series plasmids encodes a thioredoxin A, a disulfide bond isomerase, has been commonly used to improve the solubility of proteins. FIGS. 12A and 12B show the results of the SDS-PAGE gel electrophoresis of the soluble and insoluble sample fractions. As shown in FIG. 12A, thioredoxin-cIGF-I was found in both supernatant (S) and insoluble pellet (P) fractions, but most of the recombinant protein was in the pellet when the induction temperature was at from 37° C. to 20° C. The total amounts of the recombinant protein thioredoxin-cIGF-I produced (in S+P fractions) were similar when the induction temperature was at between 37° C. to 20° C., but declined dramatically at 15° C. These results indicated that thioredoxin fusion protein of cIGF-I expressed in *E. coli* host cells harboring the vector pET32b-cIGF-I was predominantly present in insoluble form. The weight ratios (S/S+P) of the soluble form (S) fusion protein versus the total fusion protein (soluble form plus insoluble form, S+P) for the recombinant protein thioredoxin A-cIGF-I were 6%, 8%, 7%, 7% and 65% at 37° C., 30° C., 25° C., 20° C., and 15° C., respectively (Table 9). Although the low temperature at 15° C. increased the percentage of soluble recombinant protein (i.e., solubility), the overall yield was lower.

Expression of J-Domain fusion protein of cIGF-I. Unlike thioredoxin fusion protein of cIGF-I, the weight ratios of soluble PTD₁-J₁-cIGF-I fusion protein increased dramatically as the induction temperature decreased from 37° C. to 15° C., as shown in FIG. 12B. The total amounts of the recombinant protein PTD₁-J₁-cIGF-I (S+P) reduced as the induction temperature was decreased from 37° C. to 20° C. Very little of PTD₁-J₁-cIGF-I fusion protein was detected at the induction temperature of 15° C. The amount of the soluble recombinant proteins expressed at various temperatures was calculated and expressed as weight ratio as shown in Table 9. The weight ratios (S/S+P) of the soluble form fusion protein (S) versus the total fusion protein (S+P) for fusion protein PTD₁-J₁-cIGF-I were 4%, 11%, 70%, 87% and 91% at 37° C., 30° C., 25° C., 20° C., and 15° C., respectively. The data in Table 9 indicates that at the temperature from 25° C. to 15° C., the weight ratio of soluble cIGF-I relative to the total proteins was significantly higher in the J-domain-containing expression system than in the thioredoxin-containing expression system.

TABLE 9

Soluble fusion protein	/Total fusion Protein (% w/w, S/S + P)				
	37° C.	30° C.	25° C.	20° C.	15° C.
PTD ₁ -J ₁ -cIGF-I	4%	11%	70%	87%	91%
Thioredoxin A-cIGF-I	6%	8%	7%	7%	65%

J-domain Enhanced Solubility of Target Protein. The yields of the PTD₁-J₁-cIGF-I fusion protein in the soluble lysate fractions at different culture temperatures were measured as follows. The amount of PTD₁-J₁-cIGF-I and thioredoxin A-cIGF-I recombinant proteins in the soluble fractions relative to the total soluble lysate proteins was measured by scanning. The peak areas of the PTD₁-J₁-cIGF-I and thioredoxin A-cIGF-I recombinant protein (soluble fraction) relative to a constitutively expressed internal protein (an internal standard from the same soluble fraction) at different culture temperature were calculated and represented as “peak area ratio,” as shown in Table 10. The data indicates that at the temperature from 37° C. to 20° C., the amounts of soluble cIGF-I were significantly higher in the J-domain-containing expression system than in the thioredoxin-containing expression system.

Although the protein solubility was increased dramatically at the lower temperature (Table 9), the amount of soluble recombinant protein PTD₁-J₁-cIGF-I decreased as the induction temperature was lowered to 20° C. or 15° C. (Table 10). This indicates that an optimal induction temperature for J-domain fused recombinant protein expression would need to be determined for each target protein expression. The estimated optimal culture temperature for expression of PTD₁-J₁-cIGF-I fusion protein was at about 25° C., as shown in FIG. 13.

TABLE 10

Peak area ratio	37° C.	30° C.	25° C.	20° C.	15° C.
PTD ₁ -J ₁ -cIGF-I	1.8	4.4	8.5	5.5	0.7
Thioredoxin A-cIGF-I	0.4	0.4	0.5	0.5	1.5

Example 13

Enhanced Immunogenicity of Recombinant Protein

Haptoglobin α -chain contains antigenic motives located at N-peptide (amino acid residues 20 to 32) and C-peptide (amino acid residues 252 to 267). Neither the N-peptide nor the C-peptide of the haptoglobin α -chain by itself was able to elicit detectable antibodies. To increase their immunogenicities, a fusion polypeptide of N and C peptides, i.e., HpNC, was fused to the carboxyl terminal end of the chimeric gene PTD₁-J₁ and expressed as a recombinant PTD₁-J₁-HpNC peptide to raise a high titer of anti-serum in animals. The immunogenicity of the anti-serum was analyzed using SDS-PAGE gel electrophoresis and Western Blotting.

Immunization of Animals with Haptoglobin Fusion Polypeptide, HpNC.

The recombinant PTD₁-J₁-HpNC peptide was isolated to immune rats to raise antibodies against human haptoglobin using the following procedure. Each rat was injected subdermally with 500 μ g recombinant polypeptide in 0.4 ml emulsified adjuvant. After three boosts, the rat serum was collected.

SDS-PAGE gel Analysis and Western Blotting. Each human serum sample (1 μ l), in duplicate, with known haptoglobin phenotypes, Hp 1-1, Hp 2-1, and Hp 2-2, was loaded onto 15% SDS polyacrylamide gel. After semi-dry electrotransfer and blocking, the PVDF membrane was charged with a 1500-fold diluted rat serum at room temperature for 2 hr followed by an application of a 2500-fold diluted HRP-coupled goat-anti-rat IgG antibody (A-9037, Sigma) at room temperature for 2 h. The signals were detected by chemiluminescence (Cat # 34080, Pierce).

Results:

There are two haptoglobin (Hp) α -chain alleles, Hp1 and Hp2, in human population. The exon 2 of the Hp1 gene is duplicated once in the Hp2 allele, and the apparent molecular weights of the secreted mature α 1 and α 2 peptide of haptoglobin were 14 kDa and 20 kDa by SDS PAGE, respectively (Rademacher & Steele 1987; Tseng et al. 2004). Human serum samples of known Hp 1-1, Hp 2-1, and Hp 2-2 phenotypes were utilized to test the rat anti-HpNC serum. The rat anti-HpNC serum could distinctly recognize 14 kDa α 1 and 20 kDa α 2 secreted forms of haptoglobin α -chain, as indicated in FIG. 14A.

The immunogenicity of the PTD₁-J₁ peptide relative to the HpNC peptide was also assayed using dot blotting analyses. The pre-immune serum and rat anti-PTD₁-J₁-HpNC serum were utilized as primary antibodies in the immuno-blotting assay. Serially diluted amounts of recombinant polypeptides PTD₁-J₁-HpNC and PTD₁-J₁ were spotted on the PVDF membrane before subsequent incubations with rat pre-immune serum or rat anti-HpNC serum and followed by HRP-conjugated goat anti-rat IgG. As shown in FIG. 14B, the lowest detectable amount of PTD₁-J₁ and PTD₁-J₁-HpNC were 1 ng and 100 pg, respectively. That is, the HpNC region of the recombinant PTD₁-J₁-HpNC polypeptide was much more immunogenic than the accompanying PTD₁-J₁ region.

The foregoing description of the exemplary embodiments of the invention has been presented only for the purposes of illustration and description and is not intended to be exhaustive or to limit the invention to the precise forms disclosed. Many modifications and variations are possible in light of the above teaching.

The embodiments and examples were chosen and described in order to explain the principles of the invention and their practical application so as to enable others skilled in the art to utilize the invention and various embodiments and with various modifications as are suited to the particular use contemplated. Alternative embodiments will become apparent to those skilled in the art to which the present invention pertains without departing from its spirit and scope. Accordingly, the scope of the present invention is defined by the appended claims rather than the foregoing description and the exemplary embodiments described therein.

Some references, which may include patents, patent applications and various publications, are cited and discussed in the description of this invention. The citation and/or discussion of such references is provided merely to clarify the description of the present invention and is not an admission that any such reference is “prior art” to the invention described herein. All references cited and discussed in this specification are incorporated herein by reference in their

entireties and to the same extent as if each reference was individually incorporated by reference.

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2. Genevax P., Georgopoulos C. and Kelley W. L. (2007) The Hsp70 chaperone machines of *Escherichia coli*: a paradigm for the repartition of chaperone functions. *Mol Microbiol*, 66, 840-57.
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8. Wadia J. S., Stan R. V. and Dowdy S. F. (2004) Transducible TAT-HA fusogenic peptide enhances escape of TAT-fusion proteins after lipid raft macropinocytosis. *Nat Med*, 10, 310-5.
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SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 68

<210> SEQ ID NO 1
 <211> LENGTH: 11
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 1 5 10

<210> SEQ ID NO 2
 <211> LENGTH: 33
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 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Human immunodeficiency virus Tat PTD1

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 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

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 20 25 30

Asp Lys Asn Lys Glu Pro Arg Ala Glu Glu Lys Phe Lys Glu Ile Ala
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Arg Tyr Gly Glu Glu Gly Leu Lys
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gaagagaaat tcaaagagat cgcagaagca tacgacgttc tgagcgatcc acgtaaactg      180
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<212> TYPE: DNA
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<223> OTHER INFORMATION: Forward primer J1 nBF1 for synthesis of HSP40
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<223> OTHER INFORMATION: Forward primer nF2 for synthesis of HSP40 J-
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<223> OTHER INFORMATION: Forward primer F3 for synthesis of HSP40 J-
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 <220> FEATURE:
 <223> OTHER INFORMATION: Forward primer F5 for synthesis of HSP40 J-domain

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 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Reverse primer EcoR1 R1 for synthesis of HSP40 J-domain

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 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
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 <223> OTHER INFORMATION: Reverse primer R3 for synthesis of HSP40 J-domain

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<210> SEQ ID NO 17
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 <212> TYPE: DNA
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 <223> OTHER INFORMATION: Human HSPA1A peptide I-encoding sequence

<400> SEQUENCE: 17

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<210> SEQ ID NO 18
 <211> LENGTH: 57
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

Ser Ser Ser Thr Gln Ala Ser Leu Glu Ile Asp Ser Leu Phe Glu Gly
 1 5 10 15

Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg Phe Glu Glu Leu Cys
 20 25 30

Ser Asp Leu Phe Arg Ser Thr Leu Glu Pro Val Glu Lys Ala Leu Arg
 35 40 45

Asp Ala Lys Leu Asp Lys Ala Gln Ile
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<210> SEQ ID NO 19
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 <212> TYPE: DNA
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 <223> OTHER INFORMATION: Forward primer RI-I-f1 for synthesis of HSPA1A peptide I

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 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Forward primer I-f2 for synthesis of HSPA1A peptide I

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<220> FEATURE:
 <223> OTHER INFORMATION: Reverse primer I-r3 for synthesis of HSPA1A peptide I

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 <223> OTHER INFORMATION: Reverse primer I-r2 for synthesis of HSPA1A peptide I

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<220> FEATURE:
 <223> OTHER INFORMATION: Reverse primer Xho-I-r1 for synthesis of HSPA1A peptide I

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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence

<220> FEATURE:
 <223> OTHER INFORMATION: Human HSPA1A peptide II-encoding sequence

<400> SEQUENCE: 25

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ttc 183

<210> SEQ ID NO 26
 <211> LENGTH: 61
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

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Val Gln Glu Ala Glu Lys Tyr Lys Ala Glu Asp Glu Val Gln Arg Glu
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Arg Val Ser Ala Lys Asn Ala Leu Glu Ser Tyr Ala Phe
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<210> SEQ ID NO 27

<211> LENGTH: 49

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer RI-II-f1 for synthesis of
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<211> LENGTH: 49

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer II-f2 for synthesis of HSPA1A
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<223> OTHER INFORMATION: Forward primer II-f3 for synthesis of HSPA1A
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<220> FEATURE:

<223> OTHER INFORMATION: Forward primer II-f4 for synthesis of HSPA1A
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<212> TYPE: DNA

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<220> FEATURE:

<223> OTHER INFORMATION: Reverse primer II-r3 for synthesis of HSPA1A
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<213> ORGANISM: Artificial Sequence

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<210> SEQ ID NO 39

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<223> OTHER INFORMATION: Reverse primer III-r3 for synthesis of HSPA1A peptide III

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Reverse primer III-r2 for synthesis of HSPA1A peptide III

<400> SEQUENCE: 41

cgggttgCG acctgttCGa gttctttacg tttatgttCGa aattcCGa 48

<210> SEQ ID NO 42

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Reverse primer III-r1 for synthesis of HSPA1A peptide III

<400> SEQUENCE: 42

ctCGagCGCG cCGtgataCGa ggCGCGtaat aatCGgggttCG cacacCGtCG 48

<210> SEQ ID NO 43

<211> LENGTH: 210

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: chicke IGF-1 encoding sequence

-continued

<400> SEQUENCE: 43

```

gggccagaaa ccctgtgtgg tgcagaactg gttgatgcac tgcagttcgt gtgtggtgat    60
cgtggtttct acttcagcaa accgactggg tatggtagct ctagccgtcg tctgcatcac    120
aaaggtattg tggatgaatg ttgctttcag agctgtgatc tgcgtcgtct ggaaatgtac    180
tgtgcaccaa tcaaaccacc gaaaagcgca                                210

```

<210> SEQ ID NO 44

<211> LENGTH: 70

<212> TYPE: PRT

<213> ORGANISM: Gallus gallus

<400> SEQUENCE: 44

```

Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe
1           5           10           15
Val Cys Gly Asp Arg Gly Phe Tyr Phe Ser Lys Pro Thr Gly Tyr Gly
20           25           30
Ser Ser Ser Ala Ala Leu His His Lys Gly Ile Val Asp Glu Cys Cys
35           40           45
Phe Gln Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Ile
50           55           60
Lys Pro Pro Lys Ser Ala
65           70

```

<210> SEQ ID NO 45

<211> LENGTH: 58

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer RI-F1 new for synthesis of cIGF-I

<400> SEQUENCE: 45

```

gaattctggt ccagaaacc tgtgtggtgc agaactggtt gatgcactgc agttcgtg    58

```

<210> SEQ ID NO 46

<211> LENGTH: 48

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer F2 for synthesis of cIGF-I

<400> SEQUENCE: 46

```

gaactggttg atgcactgca gttcgtgtgt ggtgatcgtg gtttctac    48

```

<210> SEQ ID NO 47

<211> LENGTH: 51

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer F3 for synthesis of cIGF-I

<400> SEQUENCE: 47

```

ggtgatcgtg gtttctactt cagcaaaccg actggttatg gtagctctag c    51

```

<210> SEQ ID NO 48

<211> LENGTH: 49

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer F4 for cIGF-I

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<400> SEQUENCE: 48

ggttatggta gctctagccg tcgtctgcat cacaaaggta ttgtggatg 49

<210> SEQ ID NO 49

<211> LENGTH: 50

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer F5 for cIGF-I

<400> SEQUENCE: 49

cacaaaggta ttgtggatga atgttgcttt cagagctgtg atctgcgtcg 50

<210> SEQ ID NO 50

<211> LENGTH: 45

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Reverse primer R2 for synthesis of cIGF-I

<400> SEQUENCE: 50

gattggtgca cagtacattt ccagacgacg cagatcacag ctctg 45

<210> SEQ ID NO 51

<211> LENGTH: 46

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Reverse primer Xho-R1 for synthesis of cIGF-I

<400> SEQUENCE: 51

ctcgagtgcg cttttcggtg gtttgattgg tgcacagtac atttcc 46

<210> SEQ ID NO 52

<211> LENGTH: 489

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Avian Influenza HA (H5) RBD-encoding sequence

<400> SEQUENCE: 52

aaacacctat tgagcagaat aaaccatttt gagaaaattc agatcatccc caaaagttct 60

tgggccagtc atgaagcctc attaggggtg agctcagcat gtccatacca gggaaagtcc 120

tcctttttca gaaatgtggt atggcttatt aaaaagaaca gtacataccc aacaataaag 180

aggagctaca ataataccaa ccaagaagat cttttggtac tgtgggggat tcaccatcct 240

aatgatgcgg cagagcagac aaagctctat caaaacccaa ccacctatat ttccgttggg 300

acatcaacac taaaccagag attggtacca agaatagcta ctagatccga agtaaacggg 360

caaagtggaa ggatggagt cttctggaca attttaaaac cgaatgatgc aatcaacttc 420

gagagtaatg gaaatttcat tgctccagaa tatgcataca aaattgtcaa gaaaggggac 480

tcaacaatt 489

<210> SEQ ID NO 53

<211> LENGTH: 163

<212> TYPE: PRT

<213> ORGANISM: Avian Influenza virus HA subtype H5

-continued

<400> SEQUENCE: 53

Lys His Leu Leu Ser Arg Ile Asn His Phe Glu Lys Ile Gln Ile Ile
 1 5 10 15
 Pro Lys Ser Ser Trp Ser Ser His Glu Ala Ser Leu Gly Val Ser Ser
 20 25 30
 Ala Cys Pro Tyr Gln Gly Lys Ser Ser Phe Phe Arg Asn Val Val Trp
 35 40 45
 Leu Ile Lys Lys Asn Ser Thr Tyr Pro Thr Ile Lys Arg Ser Tyr Asn
 50 55 60
 Asn Thr Asn Gln Glu Asp Leu Leu Val Leu Trp Gly Ile His His Pro
 65 70 75 80
 Asn Asp Ala Ala Glu Gln Thr Lys Leu Tyr Gln Asn Pro Thr Thr Tyr
 85 90 95
 Ile Ser Val Gly Thr Ser Thr Leu Asn Gln Arg Leu Val Pro Arg Ile
 100 105 110
 Ala Thr Arg Ser Glu Val Asn Gly Gln Ser Gly Arg Met Glu Phe Phe
 115 120 125
 Trp Thr Ile Leu Lys Pro Asn Asp Ala Ile Asn Phe Glu Ser Asn Gly
 130 135 140
 Asn Phe Ile Ala Pro Glu Tyr Ala Tyr Lys Ile Val Lys Lys Gly Asp
 145 150 155 160
 Ser Thr Ile

<210> SEQ ID NO 54

<211> LENGTH: 32

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequenece

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer RI HA-RBD f for synthesis of avian influenza HARBD

<400> SEQUENCE: 54

tgaattcgaa acacctattg agcagaataa ac 32

<210> SEQ ID NO 55

<211> LENGTH: 31

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequenece

<220> FEATURE:

<223> OTHER INFORMATION: Reverse primer Xho HA-RBD r for synthesis of avian influenza HARBD

<400> SEQUENCE: 55

tctcgagaat tggtgagtcc cctttcttga c 31

<210> SEQ ID NO 56

<211> LENGTH: 573

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequenece

<220> FEATURE:

<223> OTHER INFORMATION: Hepatitis C virus core protein-encoding sequence

<400> SEQUENCE: 56

atgagcacia atcctaaacc tcaaagaaaa accaaaagaa acaccaaccg tcgcccagaa 60

gacgttaagt tcccgggagg cggccagatc gttggcggag tataactgtt gccgcgcagg 120

ggccccaggt tgggtgtgag cagcacaagg aaaacttcgg agcgggtcca gccacgtggg 180

agacgccagc ccatcccaa agatcggcgc tccactggca aggcctgggg aaaaccaggt 240

-continued

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cgcccctggc ccctatatgg gaatgagggg ctcggctggg caggatggct cctgtccccc 300
cgaggtctct gccctcctg gggccccact gacccccggc ataggtcgcg caacgtgggt 360
aaagtcatcg acaccctaac gtgtggcttt gccgacctca tggggtacat ccccgtcgta 420
ggcgccccgc ttagtgggcg cgccagagct gtcgcgcacg gcgtgagagt cctggaggac 480
ggggttaatt atgcaacagg gaacctaccg ggtttccct tttctatctt cttgctggcc 540
ctgttgctct gcataccgt tccggctctct gct 573

```

```

<210> SEQ ID NO 57
<211> LENGTH: 191
<212> TYPE: PRT
<213> ORGANISM: Hepatitis C virus

```

```

<400> SEQUENCE: 57

```

```

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1          5          10          15
Arg Arg Pro Glu Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20          25          30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Thr
35          40          45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50          55          60
Ile Pro Lys Asp Arg Arg Ser Thr Gly Lys Ala Trp Gly Lys Pro Gly
65          70          75          80
Arg Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
85          90          95
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100         105         110
Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu Thr Cys
115         120         125
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Leu
130         135         140
Ser Gly Ala Ala Arg Ala Val Ala His Gly Val Arg Val Leu Leu Asp
145         150         155         160
Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Phe Pro Phe Ser Ile
165         170         175
Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Ala
180         185         190

```

```

<210> SEQ ID NO 58
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Forward primer RI-Core f for HCV-core protein

```

```

<400> SEQUENCE: 58

```

```

tgaattcgat gagcacaat cctaacctc 30

```

```

<210> SEQ ID NO 59
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Reverse primer Xho-Core r for for HCV-core
protein

```

-continued

<400> SEQUENCE: 59

tctcgagagc agagaccgga acggtgat 28

<210> SEQ ID NO 60

<211> LENGTH: 105

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Fusion gene encoding Human Haptoglobin Fusion Polypeptide HpNC

<400> SEQUENCE: 60

gatagcggta acgatgtgac cgatattgcg gatgatggtg gtagcgggtg tcgtcattat 60

gaaggtagca ccgttccgga gaagaaaacc ccaaagagcg gtggt 105

<210> SEQ ID NO 61

<211> LENGTH: 35

<212> TYPE: PRT

<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 61

Asp Ser Gly Asn Asp Val Thr Asp Ile Ala Asp Asp Gly Gly Ser Gly
1 5 10 15Gly Arg His Tyr Glu Gly Ser Thr Val Pro Glu Lys Lys Thr Pro Lys
20 25 30Ser Gly Gly
35

<210> SEQ ID NO 62

<211> LENGTH: 49

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer RI-F1 for Human Haptoglobin fusion polypeptide HpNC

<400> SEQUENCE: 62

agaattctga tagcggcaac gatgtgaccg atattgcgga tgatggtg 49

<210> SEQ ID NO 63

<211> LENGTH: 44

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer F2 for Human Haptoglobin fusion polypeptide HpNC

<400> SEQUENCE: 63

tgaccgatat tgcgatgat ggtggtagt gtggtcgtca ttat 44

<210> SEQ ID NO 64

<211> LENGTH: 41

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Forward primer F3 for Human Haptoglobin fusion polypeptide HpNC

<400> SEQUENCE: 64

atggtggtag tgggtggtcgt cattatgaag gtagcaccgt t 41

-continued

<210> SEQ ID NO 65
 <211> LENGTH: 47
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Reverse primer R2 for Human Haptoglobin fusion polypeptide HpNC

<400> SEQUENCE: 65

ggttttcttc tccggaacgg tgctaccttc ataatgacga ccaccac 47

<210> SEQ ID NO 66
 <211> LENGTH: 47
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Reverse primer Xho-R1 for Human Haptoglobin fusion polypeptide HpNC

<400> SEQUENCE: 66

tctcgagacc accgctcttt ggggttttct tctccggaac ggtgcta 47

<210> SEQ ID NO 67
 <211> LENGTH: 99
 <212> TYPE: DNA
 <213> ORGANISM: Oryctolagus cuniculus

<400> SEQUENCE: 67

gtggtctgtg cgtgcagacg agccctctgt ttgcctcggg aacgtcgtgc tgggttctgc 60

agaatccgtg gaagaatcca cccactctgc tgccgccgc 99

<210> SEQ ID NO 68
 <211> LENGTH: 33
 <212> TYPE: PRT
 <213> ORGANISM: Oryctolagus cuniculus

<400> SEQUENCE: 68

Val Val Cys Ala Cys Arg Arg Ala Leu Cys Leu Pro Arg Glu Arg Arg
 1 5 10 15

Ala Gly Phe Cys Arg Ile Arg Gly Arg Ile His Pro Leu Cys Cys Arg
 20 25 30

Arg

What is claimed is:

1. A chimeric protein comprising:

- (a) a first polypeptidyl fragment at the N-terminal end of the chimeric protein, comprising a protein transduction domain (PTD) having HIV Tat PTD activity; 50
- (b) a second polypeptidyl fragment at the C-terminal end of the first polypeptidyl fragment, comprising a J-domain having heat shock protein 70 (Hsp70)-interacting activity; and 55
- (c) a third polypeptidyl fragment at the C-terminal end of the second polypeptidyl fragment, comprising a target protein or polypeptide.

2. The chimeric protein of claim 1, wherein the first polypeptidyl fragment comprises the amino acid sequence of SEQ ID NO: 1.

3. The chimeric protein of claim 1, wherein the second polypeptidyl fragment comprises the amino acid sequence of SEQ ID NO: 3.

4. The chimeric protein of claim 1, wherein the J-domain is heat shock protein 40 (Hsp40) J-domain.

* * * * *